

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.39627 Seconds  
(without alignments)  
302.622 Million cell updates/sec

Title: US-09-628-112-20

Perfect score: 1992

Sequence: 1 MHFTQVLISLVLACGPVG.....KEQIIYKIPSMVVDRCGS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

1: /cgn2\_6/ptodata/1/pubpaa/US10 NEW PUB.pap.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06 NEW PUB.pap.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07 NEW PUB.pap.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08 NEW PUB.pap.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09 NEW PUB.pap.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCT NEW PUB.pap.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11 NEW PUB.pap.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60 NEW PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284.5	14.3	391	1	US-10-517-544-77
2	253	12.7	431	1	US-10-816-768-39
3	237	11.9	366	7	US-11-091-334-9
4	233	11.7	203	1	US-10-816-768-100
5	227.5	11.4	102	1	US-10-816-768-47
6	227.5	11.4	102	1	US-10-816-768-85
7	226.5	11.4	102	1	US-10-816-768-86
8	225.5	11.3	102	1	US-10-816-768-46
9	224.5	11.3	102	1	US-10-816-768-84
10	224	11.2	117	1	US-10-816-768-69
11	224	11.2	139	1	US-10-816-768-68
12	224	11.2	364	1	US-10-131-826A-342
13	224	11.2	364	7	US-11-091-334-2
14	223.5	11.2	102	1	US-10-816-768-88
15	223.5	11.2	129	1	US-10-816-768-89
16	223	11.2	429	1	US-10-967-457-74
17	220.5	11.1	102	1	US-10-816-768-53
18	219.5	11.0	106	1	US-10-816-768-62
19	219.5	11.0	106	1	US-10-816-768-63
20	216.5	10.9	102	1	US-10-816-768-83
21	216.5	10.9	102	1	US-10-816-768-87
22	212.5	10.7	98	1	US-10-816-768-41
23	212	10.6	101	1	US-10-816-768-49
24	211.5	10.6	98	1	US-10-816-768-42
25	211.5	10.6	102	1	US-10-816-768-55

26	210	10.5	101	1	US-10-816-768-59	Sequence 59, Appl
27	207.5	10.4	102	1	US-10-816-768-52	Sequence 52, Appl
28	204.5	10.3	102	1	US-10-816-768-56	Sequence 56, Appl
29	200	10.0	101	1	US-10-816-768-51	Sequence 51, Appl
30	198	9.9	103	1	US-10-816-768-50	Sequence 50, Appl
31	197.5	9.9	102	1	US-10-816-768-45	Sequence 45, Appl
32	196.5	9.9	98	1	US-10-816-768-44	Sequence 44, Appl
33	195.5	9.8	98	1	US-10-816-768-64	Sequence 64, Appl
34	189.5	9.5	98	1	US-10-816-768-64	Sequence 40, Appl
35	188.5	9.5	98	1	US-10-816-768-58	Sequence 58, Appl
36	185	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
37	181.5	9.1	102	1	US-10-816-768-57	Sequence 57, Appl
38	180.5	9.1	118	1	US-10-816-768-48	Sequence 48, Appl
39	176	8.8	35	1	US-10-816-768-9	Sequence 9, Appl
40	166	8.3	103	1	US-10-816-768-54	Sequence 54, Appl
41	147.5	7.4	102	1	US-10-816-768-60	Sequence 60, Appl
42	125.5	6.3	104	1	US-10-816-768-65	Sequence 65, Appl
43	116	5.8	105	1	US-10-816-768-61	Sequence 61, Appl
44	113	5.7	39	1	US-10-816-768-115	Sequence 115, App
45	111	5.6	39	1	US-10-816-768-119	Sequence 119, App

#### ALIGNMENTS

RESULT 1  
US-10-517-544-77  
; Sequence 77, Application US/10517544  
; Publication No. US20050250100A1  
; GENERAL INFORMATION:  
; APPLICANT: RIKEN  
; APPLICANT: KABUSHIKI KAISHA DNAFORM  
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis  
; FILE REFERENCE: 1336(PCT)  
; CURRENT APPLICATION NUMBER: US/10/517,544  
; CURRENT FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: JP 2002-171851  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: JP 2002-235294  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 77  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-517-544-77

Query Match	14.3%	Score 284.5;	DB 1;	Length 391;
Best Local Similarity	25.9%	Pred. No. 1.1e-22;		
Matches	97;	Conservative 66;	Mismatches 157;	Indels 55;
Gaps	14;			
QY	41	STCEP--RQHSKLMRLHAIKSQILSKLRLKQAPNISRDVVKKQLLPKAPLQQLLOYD--	96	
DB	31	STCKTIDMELVKRKRIEAIHQILSKLRLASPPSQE-----VPPGPLEAVLALYNST	84	
QY	97	---VLGDDSKGAVZEDDEHATTETIMTATEPDPVQVDRKPKCFPSFKIQANRTV	153	
DB	85	RDRVAGESAPEPEADYAKVTRVLMTVETHNIYDKFKQSTHSITMFTNSEUREAV	144	
QY	154	-----RAQLVWHLR---PAEEATTVFLQISRLMPVKDGGRRHRIIRSLKIDYNAVTSWQ	203	
DB	145	PEPVLLSRAELRLRLRLKLVQEHVELYQKYS-----NNSRWYLSNELLAPSDSEVL	197	
QY	204	SIDVQKVLTVMLKQETNVRGIEINAY---DAKNDLAV--TSTETGEGDGL-----P	250	
DB	198	SFDVTGVVQMLSRGSEIEGFRLSAHSCDSRDNTLQVDINGFTTGRGDLATIHGMNRP	257	
QY	251	FM-----EVKISEGPKRIRRSGLDCDB--NSSESRCRCRYLTVDP-EDFGDWIIAPKR	302	
DB	258	FLLMATPLERAQHLQSSRRRLDNTNYCFSTEKNCCVQQLYIDFRKDLGKWKWIHPKG	317	
QY	303	YKANYCSGECIDMYLQKYPHPTH---LVNKASPRGTAGPCCTPTKMSPINMLYFNKGQII	359	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.2229 Seconds  
(without alignments)  
2359.729 Million cell updates/sec

Title: US-09-628-112-20

Perfect score: 1992

Sequence: 1 MHFTQVLSLSVLIACGPVG.....KEQIIYKIPSMVDRGCS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:\*
- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*
  - 4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1992	100.0	374	3	US-09-841-730-20
2	1992	100.0	374	4	US-10-662-438-8
3	1992	100.0	374	5	US-10-665-374-8
4	1992	100.0	374	5	US-10-991-343-29
5	1989	99.8	374	4	US-10-074-152-36
6	1367.5	68.6	375	3	US-09-454-540-5
7	1367.5	68.6	375	3	US-09-859-211-14
8	1367.5	68.6	375	3	US-09-841-730-2
9	1367.5	68.6	375	3	US-09-872-856-14
10	1367.5	68.6	375	3	US-09-871-604-5
11	1367.5	68.6	375	4	US-10-074-152-29
12	1367.5	68.6	375	4	US-10-278-803-14
13	1367.5	68.6	375	4	US-10-071-499A-1
14	1367.5	68.6	375	4	US-10-335-483-14
15	1367.5	68.6	375	4	US-10-251-115-8
16	1367.5	68.6	375	4	US-10-253-532-130
17	1367.5	68.6	375	4	US-10-366-345-51
18	1367.5	68.6	375	4	US-10-463-973-14
19	1367.5	68.6	375	4	US-10-456-852-4
20	1367.5	68.6	375	4	US-10-459-127-5
21	1367.5	68.6	375	4	US-10-662-438-2
22	1367.5	68.6	375	5	US-10-689-677C-2
23	1367.5	68.6	375	5	US-10-665-374-2
24	1367.5	68.6	375	5	US-10-997-809-14
25	1367.5	68.6	375	5	US-10-991-343-14
26	1367.5	68.6	375	6	US-11-019-001-1
27	1367.5	68.6	376	3	US-09-813-398-38

28	1367.5	68.6	376	5	US-10-826-324-38	Sequence 38, Appl
29	1363.5	68.4	374	3	US-09-841-730-8	Sequence 8, Appl
30	1363.5	68.4	375	3	US-09-859-211-23	Sequence 23, Appl
31	1363.5	68.4	375	3	US-09-872-856-23	Sequence 23, Appl
32	1363.5	68.4	375	4	US-10-463-973-23	Sequence 23, Appl
33	1363.5	68.4	375	4	US-10-456-852-10	Sequence 10, Appl
34	1363.5	68.4	375	4	US-10-662-438-6	Sequence 6, Appl
35	1363.5	68.4	375	5	US-10-665-374-6	Sequence 5, Appl
36	1362.5	68.4	375	3	US-09-859-894A-5	Sequence 34, Appl
37	1360.5	68.3	375	4	US-10-074-152-34	Sequence 27, Appl
38	1358.5	68.2	375	3	US-09-859-211-27	Sequence 18, Appl
39	1358.5	68.2	375	3	US-09-841-730-18	Sequence 27, Appl
40	1358.5	68.2	375	3	US-09-872-856-27	Sequence 19, Appl
41	1358.5	68.2	375	4	US-10-278-803-19	Sequence 27, Appl
42	1358.5	68.2	375	4	US-10-463-973-27	Sequence 14, Appl
43	1358.5	68.2	375	4	US-10-456-852-14	Sequence 19, Appl
44	1357.5	68.1	375	3	US-09-859-211-19	Sequence 29, Appl
45	1357.5	68.1	375	3	US-09-859-211-29	

RESULT 1  
US-09-841-730-20  
; Sequence 20, Application US/09841730  
; Patent No. US20020157126A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS, AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME  
; FILE REFERENCE: JHU1470-2  
; CURRENT APPLICATION NUMBER: US/09/841,730  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: 09/626,896  
; PRIOR FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 09/485,046  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: PCT/US98/15598  
; PRIOR FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: 60/054,461  
; PRIOR FILING DATE: 1997-08-01  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Danio rerio  
US-09-841-730-20

Query Match 100.0%; Score 1992; DB 3; Length 374;  
Best Local Similarity 100.0%; Pred. No. 2.1e-178;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MHFTQVLSLSVLIACGPVGVDITAHQOPSTATSEELSCSTCEFRQHSKLMRLHAIKSO	60
DB	1	MHFTQVLSLSVLIACGPVGVDITAHQOPSTATSEELSCSTCEFRQHSKLMRLHAIKSO	60
QY	61	ILSKRLKQAPNISRDVVVKQLLPKAPPLQQLDDQVLDGDDSKOGAVEDEDDHATTETIM	120
DB	61	ILSKRLKQAPNISRDVVVKQLLPKAPPLQQLDDQVLDGDDSKOGAVEDEDDHATTETIM	120
QY	121	TNATEPDPVQDRKPKCCFFSPKIQANRIVRAQLWVHLRPABEATTVFQISRLMPV	180
DB	121	TNATEPDPVQDRKPKCCFFSPKIQANRIVRAQLWVHLRPABEATTVFQISRLMPV	180
QY	181	KDGGHRRISLIDYNAGVTSKQSDVKQVLTWVLKQPETNRGIGINAYDAKGNDLAVTS	240
DB	181	KDGGHRRISLIDYNAGVTSKQSDVKQVLTWVLKQPETNRGIGINAYDAKGNDLAVTS	240
QY	241	TETGDLGLPFMEVKISGPKRIRDSGLDCCDENSESSRCRCRYPLTVDPDFGWDWIAP	300

ALIGNMENTS

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.2512 Seconds  
(without alignments)  
1694.174 Million cell updates/sec

Title: US-09-628-112-20  
Perfect score: 1992  
Sequence: 1 MHFTQVLSLSVLIACGPVG.....KEQIIYKIPSMVDRCGS 374

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Issued Patents AA:\*
- 1: /cgn2\_6/prodata/1/iaa/5 COMB.pap.\*
  - 2: /cgn2\_6/prodata/1/iaa/6 COMB.pap.\*
  - 3: /cgn2\_6/prodata/1/iaa/H\_COMB.pap.\*
  - 4: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pap.\*
  - 5: /cgn2\_6/prodata/1/iaa/RE\_COMB.pap.\*
  - 6: /cgn2\_6/prodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1992	100.0	374	2	US-09-378-238-29
2	1992	100.0	374	2	US-09-626-896-20
3	1992	100.0	374	2	US-09-841-730-20
4	1989	99.8	374	2	US-09-252-149B-36
5	1367.5	68.6	375	1	US-08-525-596B-14
6	1367.5	68.6	375	1	US-08-765-875-5
7	1367.5	68.6	375	2	US-08-795-671-5
8	1367.5	68.6	375	2	US-09-177-860A-14
9	1367.5	68.6	375	2	US-09-252-149B-29
10	1367.5	68.6	375	2	US-09-378-238-14
11	1367.5	68.6	375	2	US-09-451-501-14
12	1367.5	68.6	375	2	US-09-629-938-14
13	1367.5	68.6	375	2	US-09-454-540-5
14	1367.5	68.6	375	2	US-09-686-344-14
15	1367.5	68.6	375	2	US-09-626-896-2
16	1367.5	68.6	375	2	US-09-485-046-4
17	1367.5	68.6	375	2	US-10-278-803-14
18	1367.5	68.6	375	2	US-09-841-730-2
19	1363.5	68.4	374	2	US-09-626-896-8
20	1363.5	68.4	374	2	US-09-841-730-8
21	1363.5	68.4	375	2	US-09-686-344-23
22	1363.5	68.4	375	2	US-09-485-046-10
23	1360.5	68.3	375	2	US-09-252-149B-34
24	1358.5	68.2	375	2	US-09-451-501-19
25	1358.5	68.2	375	2	US-09-686-344-27
26	1358.5	68.2	375	2	US-09-626-896-18
27	1358.5	68.2	375	2	US-09-485-046-14

28	1358.5	68.2	375	2	US-10-278-803-19	Sequence 19, Appl
29	1358.5	68.2	375	2	US-09-841-730-18	Sequence 18, Appl
30	1357.5	68.1	375	2	US-09-252-149B-30	Sequence 30, Appl
31	1357.5	68.1	375	2	US-09-686-344-19	Sequence 19, Appl
32	1357.5	68.1	375	2	US-09-686-344-29	Sequence 29, Appl
33	1357.5	68.1	375	2	US-09-626-896-10	Sequence 10, Appl
34	1357.5	68.1	375	2	US-09-626-896-14	Sequence 14, Appl
35	1357.5	68.1	375	2	US-09-485-046-6	Sequence 6, Appl
36	1357.5	68.1	375	2	US-09-841-730-10	Sequence 10, Appl
37	1357.5	68.1	375	2	US-09-841-730-14	Sequence 14, Appl
38	1355.5	68.0	375	2	US-09-252-149B-35	Sequence 35, Appl
39	1354.5	68.0	375	2	US-09-252-149B-32	Sequence 32, Appl
40	1347.5	67.6	375	2	US-09-451-501-23	Sequence 23, Appl
41	1347.5	67.6	375	2	US-10-278-803-23	Sequence 23, Appl
42	1345.5	67.5	375	2	US-09-686-344-31	Sequence 31, Appl
43	1345.5	67.5	375	2	US-09-626-896-16	Sequence 16, Appl
44	1345.5	67.5	375	2	US-09-841-730-16	Sequence 16, Appl
45	1345.5	67.5	376	1	US-08-525-596B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-09-378-238-29  
; Sequence 29, Application US/09378238  
; Patent No. 6465239  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC  
; TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN  
; TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES  
; FILE REFERENCE: JHU1120-9  
; CURRENT APPLICATION NUMBER: US/09/378, 238  
; EARLIER FILING DATE: 1999-08-19  
; EARLIER APPLICATION NUMBER: 08/795, 071  
; EARLIER FILING DATE: 1997-02-05  
; EARLIER APPLICATION NUMBER: 08/525, 596  
; EARLIER FILING DATE: 1995-10-25  
; EARLIER APPLICATION NUMBER: PCT/US94/03019  
; EARLIER FILING DATE: 1994-03-18  
; EARLIER APPLICATION NUMBER: 08/033, 923  
; EARLIER FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Danio rerio  
US-09-378-238-29

Query Match	100.0%;	Score 1992;	DB 2;	Length 374;
Best Local Similarity	100.0%;	Pred. No. 1.7e-199;		
Matches 374;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MHFTQVLSLSVLIACGPVG	DTAHQOPSTATSELSCTCFRQHSKMLRLHAIKSQ	60
Db	1	MHFTQVLSLSVLIACGPVG	DTAHQOPSTATSELSCTCFRQHSKMLRLHAIKSQ	60
Qy	61	ILSKRLKQAPNISRDVKQLLPKAP	LOQLDQYDVLGDDSKDGAVEDEHATTETIM	120
Db	61	ILSKRLKQAPNISRDVKQLLPKAP	LOQLDQYDVLGDDSKDGAVEDEHATTETIM	120
Qy	121	TMATEPDPVQDRPKCCFFSPKIQANR	IVRAQLWHLRPAEATTVFLQISRLMPV	180
Db	121	TMATEPDPVQDRPKCCFFSPKIQANR	IVRAQLWHLRPAEATTVFLQISRLMPV	180
Qy	181	KDGRHRIKSLKIDVNAVGTWSQSIDVK	QVLTWVKQPETNRGIEINAYDAKGNDLAVTS	240
Db	181	KDGRHRIKSLKIDVNAVGTWSQSIDVK	QVLTWVKQPETNRGIEINAYDAKGNDLAVTS	240
Qy	241	TETGEDGLLPFMEVKISEGPKRIRRS	GLDCDENSESSESCCRYPVLTVPDFQGWDLIAP	300

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds  
(without alignments)  
302.622 Million cell updates/sec

Title: US-09-628-112-18  
Perfect score: 2014  
Sequence: 1 MQLAVVYVYLFQMQLVHP.....KEQIIYKIPAMVDRGCS 375

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pbp:  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pbp:  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pbp:  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pbp:  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pbp:  
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7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pbp:  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pbp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312.5	15.5	391	1	US-10-517-544-77
2	257	12.8	431	1	US-10-816-768-39
3	239	11.9	429	1	US-10-967-457-74
4	236	11.7	364	1	US-10-131-826A-342
5	236	11.7	364	7	US-11-091-334-2
6	234.5	11.6	366	7	US-11-091-334-9
7	228.5	11.3	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.8	203	1	US-10-816-768-100
13	217.5	10.8	203	1	US-10-816-768-69
14	212.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.3	106	1	US-10-816-768-62
21	206.5	10.3	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.1	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.6	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.5	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.4	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.9	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.7	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.1	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1  
US-10-517-544-77  
; Sequence 77, Application US/10517544  
; Publication No. US20050250100A1  
; GENERAL INFORMATION:  
; APPLICANT: RIKEN  
; APPLICANT: KABUSHIKI KAISHA DNAFORM  
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis  
; FILE REFERENCE: 1336(PCT)  
; CURRENT APPLICATION NUMBER: US/10/517,544  
; CURRENT FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: JP 2002-171851  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: JP 2002-235294  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 77  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-517-544-77

Query Match	15.5%	Score 312.5;	DB 1;	Length 391;
Best Local Similarity	26.7%	Pred. No. 9.1e-25;		
Matches 103;	Conservative 57;	Mismatches 131;	Indels 95;	Gaps 15;
QY	49	KSRTEAIKIQILSKLRLEQAPNISRDVIKQLLPKAPLQELIDQYDVQDDSSDGLSD	108	
Db	42	KKRIETAIRGQILSKLRASPQSGE-----VPPGPLEAVLALYNSTRDRVAGESASP	95	
QY	109	D-----DYHATTET-IITMPTESDPLVQMEGKPCFFKPSFKIOYNKVVAQLWLYL--	160	
Db	96	EPEPEADYIAKEVTVLVMTVETHNEI-----YDFKQSTHSIYMPF	135	
QY	161	-----RVQKPTTVFVQILRLIKPMK-----DGTRYTGIRSLKLDMPNG	199	
Db	136	NTSELREAVPEPVLSSRAELRLRLKLVKEQHVLYQKYSNNSWRYLSNRLPLAPSDSPE	195	
QY	200	TGIWQSIDVKTVLQNLKQ-----PSNLGIEIKAPDENGCR-DLAVTF	241	
Db	196	---MLSFDTGVGVVQWLRSRGSGIEGFRLSAHCSDSDNTLQVDINGFTTGRGDUATI-	251	
QY	242	PGPGEDGLN-PPELVVRVTDTPK-----RSRRDFGLDCDEHSTESRCRYPLTVDF-BA	292	
Db	252	-----HGMNRPPILLMATPLERAQLQSRHRRALDNYCFSTENKCCVRLQYIDFRKD	306	
QY	293	FGWDWIAPKRYKANYCSGCECFVFLQKYPHTH---LVHQANPRGSAGPCCTFTKMSPN	349	

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds  
(without alignments)  
2359.729 Million cell updates/sec

Title: US-09-628-112-18

Perfect score: 2014

Sequence: 1 MQKLAVYVYILFMQILVHP.....KEQIIYGKIPAMVVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA\_Main:

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4: /cgn2\_6/prodata1/pubpaa/US10\_PUBCOMB.pgp:

5: /cgn2\_6/prodata1/pubpaa/US10B\_PUBCOMB.pgp:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2014	100.0	375	3	US-09-859-211-27 Sequence 27, Appl
2	2014	100.0	375	3	US-09-841-730-18 Sequence 18, Appl
3	2014	100.0	375	3	US-09-872-856-27 Sequence 27, Appl
4	2014	100.0	375	4	US-10-463-973-27 Sequence 27, Appl
5	2014	100.0	375	4	US-10-456-852-14 Sequence 14, Appl
6	2003	99.5	375	4	US-10-074-152-35 Sequence 35, Appl
7	1994	99.0	375	3	US-09-859-211-23 Sequence 23, Appl
8	1994	99.0	375	3	US-09-872-856-23 Sequence 23, Appl
9	1994	99.0	375	4	US-10-463-973-23 Sequence 23, Appl
10	1994	99.0	375	4	US-10-456-852-10 Sequence 10, Appl
11	1994	99.0	375	4	US-10-662-438-6 Sequence 6, Appl
12	1994	99.0	375	5	US-10-665-374-6 Sequence 6, Appl
13	1991	98.9	375	4	US-10-074-152-34 Sequence 34, Appl
14	1989	98.8	374	3	US-09-841-730-8 Sequence 8, Appl
15	1984	98.5	375	4	US-10-278-803-27 Sequence 27, Appl
16	1964	97.5	375	4	US-10-378-803-23 Sequence 23, Appl
17	1871	92.9	375	3	US-09-454-540-5 Sequence 5, Appl
18	1871	92.9	375	3	US-09-859-211-14 Sequence 14, Appl
19	1871	92.9	375	3	US-09-841-730-2 Sequence 2, Appl
20	1871	92.9	375	3	US-09-872-856-14 Sequence 14, Appl
21	1871	92.9	375	3	US-09-871-604-5 Sequence 5, Appl
22	1871	92.9	375	4	US-10-074-152-29 Sequence 29, Appl
23	1871	92.9	375	4	US-10-278-803-14 Sequence 14, Appl
24	1871	92.9	375	4	US-10-071-499A-1 Sequence 1, Appl
25	1871	92.9	375	4	US-10-335-483-14 Sequence 14, Appl
26	1871	92.9	375	4	US-10-251-115-8 Sequence 8, Appl
27	1871	92.9	375	4	US-10-253-532-130 Sequence 130, App

28	1871	92.9	375	4	US-10-366-345-51 Sequence 51, Appl
29	1871	92.9	375	4	US-10-463-973-14 Sequence 14, Appl
30	1871	92.9	375	4	US-10-456-852-4 Sequence 4, Appl
31	1871	92.9	375	4	US-10-459-127-5 Sequence 5, Appl
32	1871	92.9	375	4	US-10-662-438-2 Sequence 2, Appl
33	1871	92.9	375	5	US-10-689-677C-2 Sequence 2, Appl
34	1871	92.9	375	5	US-10-665-374-2 Sequence 2, Appl
35	1871	92.9	375	5	US-10-997-809-14 Sequence 14, Appl
36	1871	92.9	375	5	US-10-991-343-14 Sequence 14, Appl
37	1871	92.9	375	6	US-11-019-001-1 Sequence 1, Appl
38	1871	92.9	376	3	US-09-813-398-38 Sequence 38, Appl
39	1871	92.9	376	5	US-10-826-324-38 Sequence 38, Appl
40	1866	92.7	375	3	US-09-859-894A-5 Sequence 5, Appl
41	1866	92.7	375	3	US-09-859-211-29 Sequence 29, Appl
42	1866	92.7	375	3	US-09-841-730-14 Sequence 14, Appl
43	1866	92.7	375	3	US-09-872-856-29 Sequence 29, Appl
44	1866	92.7	375	4	US-10-463-973-29 Sequence 29, Appl
45	1863	92.5	375	4	US-10-074-152-32 Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-859-211-27

; Sequence 27, Application US/09859211

; Patent No. US20020157125A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin

; APPLICANT: McPherron, Alexandra C.

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8

; FILE REFERENCE: 07265/144001

; CURRENT APPLICATION NUMBER: US/09/859,211

; CURRENT FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: 09/019,070

; PRIOR FILING DATE: 1998-02-05

; PRIOR APPLICATION NUMBER: 08/862,445

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 08/847,910

; PRIOR FILING DATE: 1997-04-28

; PRIOR APPLICATION NUMBER: 08/795,071

; PRIOR FILING DATE: 1997-02-05

; PRIOR APPLICATION NUMBER: 08/525,596

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: PCT/US94/03019

; PRIOR FILING DATE: 1994-03-18

; PRIOR APPLICATION NUMBER: 08/033,923

; PRIOR FILING DATE: 1993-03-19

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 27

; LENGTH: 375

; TYPE: PRT

; ORGANISM: Meleagris gallopavo

US-09-859-211-27

Query Match 100.0%; Score 2014; DB 3; Length 375;

Best Local Similarity 100.0%; Pred. No. 2.4e-181;

Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MQKLAVYVYILFMQILVHPVALDGSQPTENAEDGLNACTWQNTKSSRIEAKIQI 60

QY 61 LSKLRLEQAPNISRDVIKOLLKAPPLQELIDQYVQRDSSDGLDDDYHATTETIT 120

Db 61 LSKLRLEQAPNISRDVIKOLLKAPPLQELIDQYVQRDSSDGLDDDYHATTETIT 120

QY 121 MPTSDPLVQMGKPKCCFKFSSKIYNNKVAQWLIVLRQVQKPTTVFVQLIRLIPM 180

Db 121 MPTSDPLVQMGKPKCCFKFSSKIYNNKVAQWLIVLRQVQKPTTVFVQLIRLIPM 180

QY 181 KDGRTRYGIRSLKLDNMNPGTWQSIDVKTVLQNLKQPSNLGIEIKAFDENGRLAVT 240

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds  
(without alignments)  
1694.174 Million cell updates/sec

Title: US-09-628-112-18  
Perfect score: 2014  
Sequence: 1 MOKLAVYVYVILFMQILVHP.....KEQIITYGIPAMVVDRCGS 375

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/1/aaa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/aaa/H COMB.pep.\*  
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5: /cgn2\_6/ptodata/1/aaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/aaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2014	100.0	375	2	US-09-686-344-27 Sequence 27, Appl
2	2014	100.0	375	2	US-09-626-896-18 Sequence 18, Appl
3	2014	100.0	375	2	US-09-485-046-14 Sequence 14, Appl
4	2014	100.0	375	2	US-09-841-730-18 Sequence 18, Appl
5	2003	99.5	375	2	US-09-252-149B-35 Sequence 35, Appl
6	1994	99.0	375	2	US-09-686-344-23 Sequence 23, Appl
7	1994	99.0	375	2	US-09-485-046-10 Sequence 10, Appl
8	1991	98.9	375	2	US-09-252-149B-34 Sequence 34, Appl
9	1989	98.8	374	2	US-09-626-896-8 Sequence 8, Appl
10	1989	98.8	374	2	US-09-841-730-8 Sequence 8, Appl
11	1984	98.5	375	2	US-09-451-501-27 Sequence 27, Appl
12	1984	98.5	375	2	US-10-278-803-27 Sequence 27, Appl
13	1964	97.5	375	2	US-09-451-501-23 Sequence 23, Appl
14	1964	97.5	375	2	US-10-278-803-23 Sequence 23, Appl
15	1871	92.9	375	1	US-08-525-596B-14 Sequence 14, Appl
16	1871	92.9	375	1	US-08-765-875-5 Sequence 5, Appl
17	1871	92.9	375	2	US-08-795-671-5 Sequence 5, Appl
18	1871	92.9	375	2	US-09-177-860A-14 Sequence 14, Appl
19	1871	92.9	375	2	US-09-252-149B-29 Sequence 29, Appl
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21	1871	92.9	375	2	US-09-451-501-14 Sequence 14, Appl
22	1871	92.9	375	2	US-09-629-938-14 Sequence 14, Appl
23	1871	92.9	375	2	US-09-454-540-5 Sequence 5, Appl
24	1871	92.9	375	2	US-09-686-344-14 Sequence 14, Appl
25	1871	92.9	375	2	US-09-626-896-2 Sequence 2, Appl
26	1871	92.9	375	2	US-09-485-046-4 Sequence 4, Appl
27	1871	92.9	375	2	US-10-278-803-14 Sequence 14, Appl

28	1871	92.9	375	2	US-09-841-730-2	Sequence 2, Appl
29	1866	92.7	375	2	US-09-686-344-29	Sequence 29, Appl
30	1866	92.7	375	2	US-09-626-896-14	Sequence 14, Appl
31	1866	92.7	375	2	US-09-841-730-14	Sequence 14, Appl
32	1863	92.5	375	2	US-09-252-149B-32	Sequence 32, Appl
33	1862	92.5	375	2	US-09-451-501-19	Sequence 19, Appl
34	1862	92.5	375	2	US-10-278-803-19	Sequence 19, Appl
35	1861	92.4	375	2	US-09-252-149B-30	Sequence 30, Appl
36	1861	92.4	375	2	US-09-686-344-19	Sequence 19, Appl
37	1861	92.4	375	2	US-09-626-896-10	Sequence 10, Appl
38	1861	92.4	375	2	US-09-485-046-6	Sequence 6, Appl
39	1861	92.4	375	2	US-09-841-730-10	Sequence 10, Appl
40	1847	91.7	376	1	US-08-525-596B-12	Sequence 12, Appl
41	1847	91.7	376	2	US-09-177-860A-12	Sequence 12, Appl
42	1847	91.7	376	2	US-08-891-789B-6	Sequence 6, Appl
43	1847	91.7	376	2	US-09-252-149B-27	Sequence 27, Appl
44	1847	91.7	376	2	US-09-378-238-12	Sequence 12, Appl
45	1847	91.7	376	2	US-09-451-501-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-09-686-344-27  
; Sequence 27, Application US/09686344  
; Patent No. 6607884  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/686,344  
; CURRENT FILING DATE: 2006-10-10  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Meleagris gallopavo  
US-09-686-344-27

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Best Local Similarity 100.0%; Pred. No. 1.4e-191;  
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	LSKLEQAPNISRDVIKQLLPKAPPLQELIDQYDVRDSDSGSLEDYHATTETIIT	120
Db	61	LSKLEQAPNISRDVIKQLLPKAPPLQELIDQYDVRDSDSGSLEDYHATTETIIT	120
Qy	121	MPTSDFLVQMEGPKCCFFKFSKIQNKVKAQLWYLRQVKPTTVFVQILRIKPM	180
Db	121	MPTSDFLVQMEGPKCCFFKFSKIQNKVKAQLWYLRQVKPTTVFVQILRIKPM	180
Qy	181	KDGTTRYTGIRSLKLDMPNFGTGIWQSIDVKTVLQNLWKQPESNLGIEIKAFDNGRDLAVT	240
Db	181	KDGTTRYTGIRSLKLDMPNFGTGIWQSIDVKTVLQNLWKQPESNLGIEIKAFDNGRDLAVT	240

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds  
(without alignments)  
302.622 Million cell updates/sec

Title: US-09-628-112-16

Perfect score: 2011

Sequence: 1 MQKLQIFVYILFMLVAGP.....KEQIIVKIPGNVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

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- 2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312.5	15.5	391	1	US-10-517-544-77
2	260	12.9	431	1	US-10-816-768-39
3	246	12.2	429	1	US-10-967-457-74
4	245.5	12.2	366	7	US-11-091-334-9
5	238.5	11.9	364	1	US-10-131-826A-342
6	238.5	11.9	364	7	US-11-091-334-2
7	230.5	11.5	102	1	US-10-816-768-47
8	223.5	11.1	102	1	US-10-816-768-53
9	222.5	11.1	102	1	US-10-816-768-46
10	221.5	11.0	102	1	US-10-816-768-100
11	220.5	11.0	129	1	US-10-816-768-89
12	220	10.9	139	1	US-10-816-768-68
13	218.5	10.9	117	1	US-10-816-768-69
14	214.5	10.7	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-55
16	212.5	10.6	102	1	US-10-816-768-86
17	212.5	10.6	102	1	US-10-816-768-88
18	211.5	10.5	102	1	US-10-816-768-84
19	211	10.5	101	1	US-10-816-768-59
20	207.5	10.3	106	1	US-10-816-768-62
21	207.5	10.3	106	1	US-10-816-768-63
22	207	10.3	101	1	US-10-816-768-49
23	206.5	10.3	102	1	US-10-816-768-83
24	205.5	10.2	98	1	US-10-816-768-41
25	205.5	10.2	102	1	US-10-816-768-52

#### ALIGNMENTS

##### RESULT 1

US-10-517-544-77  
; Sequence 77, Application US/10517544  
; Publication No. US20050250100A1  
; GENERAL INFORMATION:  
; APPLICANT: RIKEN  
; APPLICANT: KABUSHIKI KAISHA DNAFORM  
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis  
; FILE REFERENCE: 1336(PCT)  
; CURRENT APPLICATION NUMBER: US/10/517,544  
; CURRENT FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: JP 2002-171851  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: JP 2002-235294  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 77  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-517-544-77

Query Match 15.5%; Score 312.5; DB 1; Length 391;  
Best Local Similarity 27.6%; Pred No. 3.1e-24;  
Matches 102; Conservative 61; Mismatches 145; Indels 61; Gaps 15;  
QY 49 KSSLEAIKIQILSKRLLETAPNISKDAIRQLLPKAPPLRELIDQYDVORDSDSGSLED 108  
42 KKKRIEAIKQILSKRLASPPSQGE-----VPPGPLEAVLALYNSTRDRVAGESAEP 95  
QY 109 D-----DYHTTET-VITMPTSDLLAEVQEPKCCFFKFSKIQHNKY-----VKAQL 156  
96 EPEPEADYAKEVTRVLMVETHNEIYDFKQSTHSIYMPFNTSELREAVPEPVLLSRAEL 155  
QY 157 WYLRPVKPTTTFVQILRLIKPMKDGTRYTGIRSLKIDMNPCTGIWQSIDVKTQLQNW 216  
156 RL-LRRLKLVQEHVELYQ--KYSNNSWRYLNRLLAPSDSPSPE---WLSFDVTGVVRQWL 209  
QY 217 KQESNLGIEIKA-----LDENGH-----DLAVTFPPPEBEGLN-PPLEVKV 257  
210 SRGGIEGRFLSAHSCDSRDNTLQVDINGFTTGRGDLATI-----HGMNRPFLLLMA 263  
QY 258 TDTPK-----RSRRDFGLDCDEHSTSRCCRYPLTVDF-EAFGWDWIIAPRYKANYC 309  
264 TPLRAQHLQSSRRHRALDNTNYCFSSTEKNCCVRLQYIDFRKDLGKWKIHEPKGYHANFC 323  
QY 310 SECEFFLQKYPHPTH---LVHQNPKGSAAGCCTPTKMSPINMLYFNGKEIYKIPG 366

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds  
(without alignments)  
2359.729 Million cell updates/sec

Title: US-09-628-112-16

Perfect score: 2011

Sequence: 1 MQKLIQFVYIYLFMLLVAGP.....KEQIIYKIGMVVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2011	100.0	375	3	US-09-859-211-31
2	2011	100.0	375	3	US-09-841-730-16
3	2011	100.0	375	3	US-09-872-856-31
4	2011	100.0	375	4	US-10-463-973-31
5	2008	99.9	375	4	US-10-074-152-33
6	1943	96.6	375	3	US-08-859-211-29
7	1943	96.6	375	3	US-09-841-730-14
8	1943	96.6	375	3	US-09-872-856-29
9	1943	96.6	375	4	US-10-463-973-29
10	1940	96.5	375	4	US-10-074-152-32
11	1917	95.3	375	3	US-09-454-540-5
12	1917	95.3	375	3	US-08-859-211-14
13	1917	95.3	375	3	US-09-841-730-2
14	1917	95.3	375	3	US-09-872-856-14
15	1917	95.3	375	3	US-09-871-604-5
16	1917	95.3	375	4	US-10-074-152-29
17	1917	95.3	375	4	US-10-278-803-14
18	1917	95.3	375	4	US-10-071-499A-1
19	1917	95.3	375	4	US-10-335-483-14
20	1917	95.3	375	4	US-10-251-115-8
21	1917	95.3	375	4	US-10-253-532-130
22	1917	95.3	375	4	US-10-366-345-51
23	1917	95.3	375	4	US-10-463-973-14
24	1917	95.3	375	4	US-10-456-852-4
25	1917	95.3	375	4	US-10-459-127-5
26	1917	95.3	375	4	US-10-662-438-2
27	1917	95.3	375	5	US-10-689-677C-2

28	1917	95.3	375	5	US-10-665-374-2	Sequence 2, Appl
29	1917	95.3	375	5	US-10-997-809-14	Sequence 14, Appl
30	1917	95.3	375	5	US-10-991-343-14	Sequence 14, Appl
31	1917	95.3	375	6	US-11-019-001-1	Sequence 1, Appl
32	1917	95.3	376	3	US-09-813-398-38	Sequence 38, Appl
33	1917	95.3	376	5	US-10-826-324-38	Sequence 19, Appl
34	1916	95.3	375	4	US-10-278-803-19	Sequence 19, Appl
35	1915	95.2	375	3	US-09-859-211-19	Sequence 19, Appl
36	1915	95.2	375	3	US-09-841-730-10	Sequence 19, Appl
37	1915	95.2	375	3	US-09-872-856-19	Sequence 19, Appl
38	1915	95.2	375	4	US-10-074-152-30	Sequence 30, Appl
39	1915	95.2	375	4	US-10-463-973-19	Sequence 19, Appl
40	1915	95.2	375	4	US-10-456-852-6	Sequence 6, Appl
41	1912	95.1	375	3	US-09-859-894A-5	Sequence 5, Appl
42	1892	94.1	375	4	US-10-278-803-21	Sequence 21, Appl
43	1890	94.0	375	3	US-09-859-211-21	Sequence 21, Appl
44	1890	94.0	375	3	US-09-841-730-12	Sequence 12, Appl
45	1890	94.0	375	3	US-09-872-856-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-09-859-211-31  
; Sequence 31, Application US/09859211  
; Patent No. US20020157125A1  
; GENERAL INFORMATION:  
; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/859,211  
; CURRENT FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/019,070  
; PRIOR FILING DATE: 1998-02-05  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Ovine  
US-09-859-211-31

Query Match	100.0%	Score	2011;	DB	3;	Length	375;
Best Local Similarity	100.0%	Pred. No.	2.7e-180;				
Matches	375;	Conservative	0;	Mismatches	0;	Gaps	0;
Qy	1	MQKLIQFVYIYLFMLLVAGPVDLNENSEKENVKGLCNACLRQNNKSRLEAIKIQI	60				
Db	1	MQKLIQFVYIYLFMLLVAGPVDLNENSEKENVKGLCNACLRQNNKSRLEAIKIQI	60				
Qy	61	LSKRLTETAPNISKDAIRQLLPKAPPLRELIQDVQDRDSSDGLDDDDYVHTTETVIT	120				
Db	61	LSKRLTETAPNISKDAIRQLLPKAPPLRELIQDVQDRDSSDGLDDDDYVHTTETVIT	120				
Qy	121	MPETSDLLAEVQSKPKCCPFKSSKIQHNKVQAQLMIYLRPVKTPPTVFQILRLKPM	180				
Db	121	MPETSDLLAEVQSKPKCCPFKSSKIQHNKVQAQLMIYLRPVKTPPTVFQILRLKPM	180				
Qy	181	KDGTTRYTGIRSLKLDMMNPGTGIWQSIDKVTQLQNLKQPESNLGIEIKALDENGHLAVT	240				



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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds  
(without alignments)  
1694.174 Million cell updates/sec

Title: US-09-628-112-16

Perfect score: 2011

Sequence: 1 MOKLQIFVYIYLFMLLVAGP.....KEIYKIPGMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2011	100.0	375	2	US-09-686-344-31
2	2011	100.0	375	2	US-09-626-896-16
3	2011	100.0	375	2	US-09-841-730-16
4	2008	99.9	375	2	US-09-252-1498-33
5	1943	96.6	375	2	US-09-686-344-29
6	1943	96.6	375	2	US-09-626-896-14
7	1943	96.6	375	2	US-09-841-730-14
8	1940	96.5	375	2	US-09-252-1498-32
9	1917	95.3	375	1	US-08-525-596B-14
10	1917	95.3	375	1	US-08-765-875-5
11	1917	95.3	375	2	US-08-795-671-5
12	1917	95.3	375	2	US-09-177-860A-14
13	1917	95.3	375	2	US-09-252-1498-29
14	1917	95.3	375	2	US-09-378-238-14
15	1917	95.3	375	2	US-09-451-501-14
16	1917	95.3	375	2	US-09-629-938-14
17	1917	95.3	375	2	US-09-454-540-5
18	1917	95.3	375	2	US-09-686-344-14
19	1917	95.3	375	2	US-09-626-896-2
20	1917	95.3	375	2	US-09-485-046-4
21	1917	95.3	375	2	US-10-278-803-14
22	1917	95.3	375	2	US-09-841-730-2
23	1916	95.3	375	2	US-09-451-501-19
24	1916	95.3	375	2	US-10-278-803-19
25	1915	95.2	375	2	US-09-252-1498-30
26	1915	95.2	375	2	US-09-686-344-19
27	1915	95.2	375	2	US-09-626-896-10

28	1915	95.2	375	2	US-09-485-046-6	Sequence 6, Appl
29	1915	95.2	375	2	US-09-841-730-10	Sequence 10, Appl
30	1892	94.1	375	2	US-09-451-501-21	Sequence 21, Appl
31	1892	94.1	375	2	US-10-278-803-21	Sequence 21, Appl
32	1890	94.0	375	2	US-08-891-789B-2	Sequence 2, Appl
33	1890	94.0	375	2	US-09-686-344-21	Sequence 21, Appl
34	1890	94.0	375	2	US-09-626-896-12	Sequence 12, Appl
35	1890	94.0	375	2	US-09-485-046-8	Sequence 8, Appl
36	1890	94.0	375	2	US-09-841-730-12	Sequence 12, Appl
37	1890	94.0	376	1	US-08-525-596B-12	Sequence 12, Appl
38	1890	94.0	376	2	US-09-177-860A-12	Sequence 12, Appl
39	1890	94.0	376	2	US-08-891-789B-6	Sequence 6, Appl
40	1890	94.0	376	2	US-09-252-1498-27	Sequence 27, Appl
41	1890	94.0	376	2	US-09-378-238-12	Sequence 12, Appl
42	1890	94.0	376	2	US-09-451-501-12	Sequence 12, Appl
43	1890	94.0	376	2	US-09-629-938-12	Sequence 12, Appl
44	1890	94.0	376	2	US-09-686-344-12	Sequence 12, Appl
45	1890	94.0	376	2	US-09-626-896-4	Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-09-686-344-31  
; Sequence 31, Application US/09686344  
; Patent No. 6607884  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/686,344  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Ovine  
US-09-686-344-31

Query Match						100.0%; Score 2011; DB 2; Length 375;
Best Local Similarity						100.0%; Pred. No. 4.2e-185;
Matches						375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MOKLQIFVYIYLFMLLVAGPVDL	NSESKENVEKKGKLCNACLMFQNNKSSRLBAIKIQI	60		
Db	1	MOKLQIFVYIYLFMLLVAGPVDL	NSESKENVEKKGKLCNACLMFQNNKSSRLBAIKIQI	60		
QY	61	LSKRLTAPNISDQATROLIPKAPPLREL	DDQVDVDRDSDSGSLEDDDDVHVTETVIT	120		
Db	61	LSKRLTAPNISDQATROLIPKAPPLREL	DDQVDVDRDSDSGSLEDDDDVHVTETVIT	120		
QY	121	MPTESDLIAEVOEKPKCCFFKSSKI	QHNKVVAQWLVIYLRPVKTPTTVFVQILRLIKPM	180		
Db	121	MPTESDLIAEVOEKPKCCFFKSSKI	QHNKVVAQWLVIYLRPVKTPTTVFVQILRLIKPM	180		
QY	181	KDGRYTGIRSLKLDMPGTGQISIDVKT	VLQNLWKQPESNLGIEIKALDENGHDLA	240		
Db	181	KDGRYTGIRSLKLDMPGTGQISIDVKT	VLQNLWKQPESNLGIEIKALDENGHDLA	240		

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds  
(without alignments)  
302.622 Million cell updates/sec

Title: US-09-628-112-14

Perfect score: 2013

Sequence: 1 MQLQIYVYIVLFLIVAGP.....KEQIIYKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308.5	15.3	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	236.5	11.7	366	7	US-11-091-334-9
4	233	11.6	429	1	US-10-967-457-74
5	232	11.5	364	1	US-10-131-826A-342
6	232	11.5	364	7	US-11-091-334-2
7	228.5	11.4	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.9	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.3	106	1	US-10-816-768-62
21	206.5	10.3	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-55
25	203.5	10.1	102	1	US-10-816-768-83

ALIGNMENTS

RESULT 1

US-10-517-544-77  
; Sequence 77, Application US/10517544  
; Publication No. US20050250100A1  
; GENERAL INFORMATION:  
; APPLICANT: RIKEN  
; APPLICANT: KANISHIKI KAISHA DNAFORM  
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis  
; FILE REFERENCE: 1336(PCT)  
; CURRENT APPLICATION NUMBER: US/10/517,544  
; CURRENT FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: JP 2002-171851  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: JP 2002-235294  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 77  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-517-544-77

Query Match 15.3%; Score 308.5; DB 1; Length 391;  
Best Local Similarity 26.7%; Pred No. 2.1e-24;  
Matches 103; Conservative 57; Mismatches 131; Indels 95; Gaps 15;  
QY 49 KSSRLAIIKIQILSKRLTAPNISKDAIRQLKAPPLRELIDQYVORDSDSGSLD 108  
Db 42 KRKRIEAIKQILSKRLASPPSQE-----VPPGPLEAVLALYNGTRDRVAGESAEP 95  
QY 109 D-----DYHATET-IITMPESDILLMOVEKPKCCFKFSSKIQYKVKVLAQWLYL-- 160  
Db 96 EPEPEADYAKVETRVLMVETHEI-----YDKFKSTHGIYMPF 135  
QY 161 -----RPVKPTTVFVQILRLIKPMK-----DGTRYTGIRSLKLDMPG 199  
Db 136 NTSELRAPVPEVLSRAELRLRLKLVQHVHLYKYNNWRYLSNRLAASDSFE 195  
QY 200 TGIWQSIDVKTVLQWNLKQPSNLGIEIKA-----LDENGH-----DLAVTF 241  
Db 196 ---NLSFDVTGVVQWLSRGGEISGFRLSAHCSDSDRNTLQVDINGFTTGRGDLATI- 251  
QY 242 PGPGEDGLN-PFLEVKVTDTPK-----RSRRDFGLDCDEHSTESRCRPLTVDF-EA 292  
Db 252 -----HGNRPFLLIMATPLERAQHLQSRHRAIDTNYCFSTKNCCKVRLYIDFRK 306  
QY 293 FGMDWIIAPKRYKANYCSGCEFFVLQKYPTH-----LVHQANPRGSAGPCCTPTTQMSPIN 349

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds  
(without alignments)  
2359.729 Million cell updates/sec

Title: US-09-628-112-14  
Perfect score: 2013  
Sequence: 1 MQLQIYVYIYLFMLIVAGP.....KEQIYKIPAMVDRGCS 375

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pcp.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pcp.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2013	100.0	375	3	US-09-859-211-29	Sequence 29, Appl
2	2013	100.0	375	3	US-09-841-730-14	Sequence 14, Appl
3	2013	100.0	375	3	US-09-872-856-29	Sequence 29, Appl
4	2013	100.0	375	4	US-10-463-973-29	Sequence 29, Appl
5	2010	99.9	375	4	US-10-074-152-32	Sequence 32, Appl
6	1979	98.3	375	3	US-09-454-540-5	Sequence 5, Appl
7	1979	98.3	375	3	US-09-859-211-14	Sequence 14, Appl
8	1979	98.3	375	3	US-09-841-730-2	Sequence 2, Appl
9	1979	98.3	375	3	US-09-872-856-14	Sequence 14, Appl
10	1979	98.3	375	3	US-09-871-604-5	Sequence 5, Appl
11	1979	98.3	375	4	US-10-074-152-29	Sequence 29, Appl
12	1979	98.3	375	4	US-10-278-803-14	Sequence 14, Appl
13	1979	98.3	375	4	US-10-071-499A-1	Sequence 1, Appl
14	1979	98.3	375	4	US-10-335-483-14	Sequence 14, Appl
15	1979	98.3	375	4	US-10-251-115-8	Sequence 8, Appl
16	1979	98.3	375	4	US-10-253-532-130	Sequence 130, App
17	1979	98.3	375	4	US-10-366-345-51	Sequence 51, Appl
18	1979	98.3	375	4	US-10-463-973-14	Sequence 14, Appl
19	1979	98.3	375	4	US-10-456-852-4	Sequence 4, Appl
20	1979	98.3	375	4	US-10-459-127-5	Sequence 5, Appl
21	1979	98.3	375	4	US-10-662-438-2	Sequence 2, Appl
22	1979	98.3	375	5	US-10-689-677C-2	Sequence 2, Appl
23	1979	98.3	375	5	US-10-665-374-2	Sequence 2, Appl
24	1979	98.3	375	5	US-10-997-809-14	Sequence 14, Appl
25	1979	98.3	375	5	US-10-991-343-14	Sequence 14, Appl
26	1979	98.3	375	6	US-11-019-001-1	Sequence 1, Appl
27	1979	98.3	376	3	US-09-813-398-38	Sequence 38, Appl

28	1979	98.3	376	5	US-10-826-324-38	Sequence 38, Appl
29	1978	98.3	375	4	US-10-278-803-19	Sequence 19, Appl
30	1977	98.2	375	3	US-09-859-211-19	Sequence 19, Appl
31	1977	98.2	375	3	US-09-841-730-10	Sequence 10, Appl
32	1977	98.2	375	3	US-09-872-856-19	Sequence 19, Appl
33	1977	98.2	375	4	US-10-074-152-30	Sequence 30, Appl
34	1977	98.2	375	4	US-10-463-973-19	Sequence 19, Appl
35	1977	98.2	375	4	US-10-456-852-6	Sequence 6, Appl
36	1974	98.1	375	3	US-09-859-894A-5	Sequence 5, Appl
37	1956	97.2	376	3	US-09-859-894A-11	Sequence 11, Appl
38	1956	97.2	376	3	US-09-859-211-12	Sequence 12, Appl
39	1956	97.2	376	3	US-09-841-730-4	Sequence 4, Appl
40	1956	97.2	376	3	US-09-872-856-12	Sequence 12, Appl
41	1956	97.2	376	3	US-09-871-604-10	Sequence 10, Appl
42	1956	97.2	376	4	US-10-074-152-27	Sequence 27, Appl
43	1956	97.2	376	4	US-10-278-803-12	Sequence 12, Appl
44	1956	97.2	376	4	US-10-335-483-12	Sequence 12, Appl
45	1956	97.2	376	4	US-10-251-115-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-09-859-211-29  
; Sequence 29, Application US/09859211  
; Patent No. US20020157125A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/859,211  
; CURRENT FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/019,070  
; PRIOR FILING DATE: 1998-02-05  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Porcine  
US-09-859-211-29

Query Match	100.0%	Score	2013;	DB	3;	Length	375;
Best Local Similarity	100.0%	Pred. No.	8.1e-183;				
Matches	375;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MQLQIYVYIYLFMLIVAGPVDLNENSEQKENVKEGLCNACMRQNTKSSRLBAIKQI	60				
Qy	61	LSKRLLETAPNISKDAIRQLLPKAPPLRELIDQYDVRDSSDGSLEDDDDYHATTETIIT	120				
Db	61	LSKRLLETAPNISKDAIRQLLPKAPPLRELIDQYDVRDSSDGSLEDDDDYHATTETIIT	120				
Qy	121	MPTESDILLMQVEGPKCCFFKFSKSIQNKVKVQAQLMIYLRPVKTPTTVFVQILRLIKPM	180				
Db	121	MPTESDILLMQVEGPKCCFFKFSKSIQNKVKVQAQLMIYLRPVKTPTTVFVQILRLIKPM	180				
Qy	181	KDGTFTYTGIRSLKLDMPNPGTGIWQSIDVKTVQLQNLKQPESNLGIEIKALDENGHLAVT	240				

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds  
(without alignments)  
1694.174 Million cell updates/sec

Title: US-09-628-112-14

Perfect score: 2013

Sequence: 1 MQKLQIYVYIYLFMLIVAGP.....KEQIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.\*
- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/PCUS\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2013	100.0	375	2	US-09-686-344-29
2	2013	100.0	375	2	US-09-626-896-14
3	2013	100.0	375	2	US-09-841-730-14
4	2010	99.9	375	2	US-09-252-149B-32
5	1979	98.3	375	1	US-08-525-596B-14
6	1979	98.3	375	1	US-08-785-875-5
7	1979	98.3	375	2	US-08-795-671-5
8	1979	98.3	375	2	US-09-177-860A-14
9	1979	98.3	375	2	US-09-252-149B-29
10	1979	98.3	375	2	US-09-378-238-14
11	1979	98.3	375	2	US-09-451-501-14
12	1979	98.3	375	2	US-09-629-938-14
13	1979	98.3	375	2	US-09-454-540-5
14	1979	98.3	375	2	US-09-686-344-14
15	1979	98.3	375	2	US-09-626-896-2
16	1979	98.3	375	2	US-09-485-046-4
17	1979	98.3	375	2	US-10-278-803-14
18	1979	98.3	375	2	US-09-841-730-2
19	1978	98.3	375	2	US-09-451-501-19
20	1978	98.3	375	2	US-10-278-803-19
21	1977	98.2	375	2	US-09-252-149B-30
22	1977	98.2	375	2	US-09-686-344-19
23	1977	98.2	375	2	US-09-626-896-10
24	1977	98.2	375	2	US-09-485-046-6
25	1977	98.2	375	2	US-09-841-730-10
26	1956	97.2	376	1	US-08-525-596B-12
27	1956	97.2	376	2	US-09-177-860A-12

28	1956	97.2	376	2	US-08-891-789B-6	Sequence 6, Appli
29	1956	97.2	376	2	US-09-252-149B-27	Sequence 27, Appl
30	1956	97.2	376	2	US-09-378-238-12	Sequence 12, Appl
31	1956	97.2	376	2	US-09-451-501-12	Sequence 12, Appl
32	1956	97.2	376	2	US-09-629-938-12	Sequence 12, Appl
33	1956	97.2	376	2	US-09-686-344-12	Sequence 12, Appl
34	1956	97.2	376	2	US-09-626-896-4	Sequence 4, Appli
35	1956	97.2	376	2	US-09-485-046-2	Sequence 2, Appli
36	1956	97.2	376	2	US-10-278-803-12	Sequence 12, Appl
37	1956	97.2	376	2	US-09-841-730-4	Sequence 4, Appli
38	1943	96.5	375	2	US-09-686-344-31	Sequence 31, Appl
39	1943	96.5	375	2	US-09-626-896-16	Sequence 16, Appl
40	1943	96.5	375	2	US-09-841-730-16	Sequence 16, Appl
41	1940	96.4	375	2	US-09-252-149B-33	Sequence 33, Appl
42	1929	95.8	375	2	US-09-451-501-21	Sequence 21, Appl
43	1929	95.8	375	2	US-10-278-803-21	Sequence 21, Appl
44	1928	95.8	376	2	US-09-252-149B-28	Sequence 28, Appl
45	1928	95.8	376	2	US-09-451-501-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-09-686-344-29  
; Sequence 29, Application US/09686344  
; Patent No. 6607884  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: McPherson, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/686,344  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Porcine

Query Match 100.0%; Score 2013; DB 2; Length 375;  
Best Local Similarity 100.0%; Pred. No. 9.2e-188;  
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQKLQIYVYIYLFMLIVAGPVDLNENSEQKENVKEGLCNACMRQNTKS9RLLEAIKIQI	60
Db	1	MQKLQIYVYIYLFMLIVAGPVDLNENSEQKENVKEGLCNACMRQNTKS9RLLEAIKIQI	60
Qy	61	LSKLRLTAPNISKDAIRQLLPKAPPLRELIDQVDORDDSSDGSLEDDDHATTETIT	120
Db	61	LSKLRLTAPNISKDAIRQLLPKAPPLRELIDQVDORDDSSDGSLEDDDHATTETIT	120
Qy	121	MPTESDLLLMQVEGKPKCCFFKSSKIYQNVKVAQLWIYLRPVKPTPTTVFVQILRLIKPM	180
Db	121	MPTESDLLLMQVEGKPKCCFFKSSKIYQNVKVAQLWIYLRPVKPTPTTVFVQILRLIKPM	180
Qy	181	KDGTRYTGIRSLKLDNMNPGTGIWQSIDVKTVLQNLWKQPSNLGIRIKALDENGHDLA	240
Db	181	KDGTRYTGIRSLKLDNMNPGTGIWQSIDVKTVLQNLWKQPSNLGIRIKALDENGHDLA	240

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds  
(without alignments)  
302.622 Million cell updates/sec

Title: US-09-628-112-12

Perfect score: 2003

Sequence: 1 MQLQISVVIYLFMLIVAGP.....EQIIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292.5	14.6	391	1	US-10-517-544-77
2	255	12.7	431	1	US-10-816-768-39
3	248.5	12.4	366	7	US-11-091-334-9
4	239.5	12.0	364	1	US-10-131-826A-342
5	239.5	12.0	364	7	US-11-091-334-2
6	228.5	11.4	102	1	US-10-816-768-47
7	225	11.2	429	1	US-10-967-457-74
8	221.5	11.1	102	1	US-10-816-768-53
9	219.5	11.0	129	1	US-10-816-768-89
10	219	10.9	139	1	US-10-816-768-68
11	218.5	10.9	203	1	US-10-816-768-100
12	217.5	10.8	117	1	US-10-816-768-69
13	216.5	10.8	102	1	US-10-816-768-46
14	212.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.5	102	1	US-10-816-768-84
18	209.5	10.5	102	1	US-10-816-768-88
19	208	10.4	101	1	US-10-816-768-59
20	203.5	10.2	102	1	US-10-816-768-52
21	203.5	10.2	102	1	US-10-816-768-56
22	203.5	10.2	102	1	US-10-816-768-83
23	202.5	10.1	102	1	US-10-816-768-87
24	202.5	10.1	106	1	US-10-816-768-62
25	202.5	10.1	106	1	US-10-816-768-63

ALIGNMENTS

RESULT 1

US-10-517-544-77

; Sequence 77, Application US/10517544

; Publication No. US20050250100A1

; GENERAL INFORMATION:

; APPLICANT: RIKEN

; APPLICANT: KABUSHIKI KAISHA DNAFORM

; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis

; FILE REFERENCE: 1336(PCT)

; CURRENT APPLICATION NUMBER: US/10/517,544

; CURRENT FILING DATE: 2004-12-10

; PRIOR APPLICATION NUMBER: JP 2002-171851

; PRIOR FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: JP 2002-235294

; PRIOR FILING DATE: 2002-08-12

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: Patent version 3.1

; SEQ ID NO 77

; LENGTH: 391

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-517-544-77

Query Match 14.6%; Score 292.5; DB 1; Length 391;

Best Local Similarity 26.4%; Pred. No. 1.9e-23;

Matches 101; Conservative 56; Mismatches 131; Indels 95; Gaps 15;

QY 52 RUEAIKIQILSKRLKETAPNISKDAIRQLLPKAPPELLELDQFDVORDASSDGSLEDD-- 109

Db 45 RTEAIRGQILSKRLASPPSQGE-----VPPGPLEAVLALYNSTRDRVAGESAPPE 98

QY 110 ---DYHARTET-VITMPTIESDLTTQVEGKPKCCFFKFSKIOYNKLVAKQLMTYL----- 160

Db 99 PEADYAYAKEVTVLMVETHNEI-----YDKFKQSTHSIYMFNTS 138

QY 161 ---RPVKPATPVFQILRLIKPMK-----DGTRYTGIRSLKLDMPGTGI 202

Db 139 ELREAVPEVLLSRAELRLRLKLVQEHVELYQKYSNNRYLSNRLAPSDEP--- 195

QY 203 WQSIDVKTVLQNLWKOPESNLGIEIKA-----LDENGH-----DLAVTFPEP 244

Db 196 WLSFDVTVGVVRQWLSRGGEIEGFRLSAHCSDSRDNTLQWDINGFTTGRGDLATI--- 251

QY 245 GEDGILT-PELEVKYVTDTPK-----RSRRDFGLDCDEHSTESRCRYPLTVDFP-SAFGW 295

Db 252 --HGMNRPPELLMATPELEAQLQSSRRHRLADNTYCFSSKNCNCVROLYIDFRKDLGW 309

QY 296 DWIAPKPKYKANCYSGCECFVFLQKYPHTH---LVHQANPRGSAGPCCTPTTKMSPINMPLY 352

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds  
(without alignments)  
2359.729 Million cell updates/sec

Title: US-09-628-112-12

Perfect score: 2003

Sequence: 1 MQLQISVYIYLFMLIVAGP.....EQIYIGKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2003	100.0	375	3	US-09-859-211-21
2	2003	100.0	375	3	US-09-841-730-12
3	2003	100.0	375	3	US-09-872-856-21
4	2003	100.0	375	4	US-10-251-115-2
5	2003	100.0	375	4	US-10-463-973-21
6	2003	100.0	375	4	US-10-456-852-8
7	2003	100.0	375	5	US-10-662-438-4
8	2003	100.0	375	5	US-10-665-374-4
9	2000	99.9	375	4	US-10-074-152-31
10	1997	99.7	375	4	US-10-074-152-2
11	1973	98.5	375	4	US-10-278-803-21
12	1927	96.2	375	3	US-09-859-211-29
13	1927	96.2	375	3	US-09-841-730-14
14	1927	96.2	375	3	US-09-872-856-29
15	1927	96.2	375	4	US-10-463-973-29
16	1924	96.1	375	4	US-10-074-152-32
17	1906	95.2	375	3	US-09-454-540-5
18	1906	95.2	375	3	US-09-859-211-14
19	1906	95.2	375	3	US-09-841-730-2
20	1906	95.2	375	3	US-09-872-856-14
21	1906	95.2	375	3	US-09-871-604-5
22	1906	95.2	375	4	US-10-074-152-29
23	1906	95.2	375	4	US-10-278-803-14
24	1906	95.2	375	4	US-10-071-499A-1
25	1906	95.2	375	4	US-10-335-483-14
26	1906	95.2	375	4	US-10-251-115-8
27	1906	95.2	375	4	US-10-253-532-130

ALIGNMENTS

RESULT 1

US-09-859-211-21  
; Sequence 21, Application US/09859211  
; Patent No. US20020157125A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/859,211  
; CURRENT FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/019,070  
; PRIOR FILING DATE: 1998-02-05  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Bovine  
US-09-859-211-21

Query Match 100.0%; Score 2003; DB 3; Length 375;

Best Local Similarity 100.0%; Pred. No. 1.9e-103; Indels 0; Gaps 0;  
Matches 375; Conservative 0; Mismatches 0;

Qy	1	MQLQISVYIYLFMLIVAGPVVDLNENSKENVEKEGLCNACLWRENTTSSRLAIIQI	60
Db	1	MQLQISVYIYLFMLIVAGPVVDLNENSKENVEKEGLCNACLWRENTTSSRLAIIQI	60
Qy	61	LSKRLLETAPNISKDAIRQLLPKAPPLLELIDQDFVQRDASDGSLEDDDYHARTETVT	120
Db	61	LSKRLLETAPNISKDAIRQLLPKAPPLLELIDQDFVQRDASDGSLEDDDYHARTETVT	120
Qy	121	MPTESDLITQVEGPKCCFFKFSKIQYNKLVKAQLWYLPVKTPATVFOVQLRLIKPM	180
Db	121	MPTESDLITQVEGPKCCFFKFSKIQYNKLVKAQLWYLPVKTPATVFOVQLRLIKPM	180
Qy	181	KDGRYTGIRSLKLDMPNPGTGIWQSIDVKTQLNWLKQPESNLGIEIKALDENGHDLA	240

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds  
(without alignments)  
1694.174 Million cell updates/sec

Title: US-09-628-112-12

Perfect score: 2003

Sequence: 1 MOKLQISVYIVFLMVLVAGP.....EGQIYIKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/ptodata/1/iaa/6 COMB pep:.\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB pep:.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB pep:.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB pep:.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2003	100.0	375	2	US-08-891-789B-2
2	2003	100.0	375	2	US-09-686-344-21
3	2003	100.0	375	2	US-09-626-896-12
4	2003	100.0	375	2	US-09-485-046-8
5	2003	100.0	375	2	US-09-841-730-12
6	2000	99.9	375	2	US-09-252-149B-31
7	1997	99.7	375	2	US-09-252-149B-2
8	1973	98.5	375	2	US-09-451-501-21
9	1973	98.5	375	2	US-10-278-803-21
10	1927	96.2	375	2	US-09-686-344-29
11	1927	96.2	375	2	US-09-626-896-14
12	1927	96.1	375	2	US-09-841-730-14
13	1924	96.1	375	2	US-09-252-149B-32
14	1906	95.2	375	1	US-08-525-596B-14
15	1906	95.2	375	1	US-08-765-875-5
16	1906	95.2	375	2	US-08-795-671-5
17	1906	95.2	375	2	US-09-177-860A-14
18	1906	95.2	375	2	US-09-252-149B-29
19	1906	95.2	375	2	US-09-378-238-14
20	1906	95.2	375	2	US-09-451-501-14
21	1906	95.2	375	2	US-09-629-938-14
22	1906	95.2	375	2	US-09-454-540-5
23	1906	95.2	375	2	US-09-686-344-14
24	1906	95.2	375	2	US-09-626-896-2
25	1906	95.2	375	2	US-09-485-046-4
26	1906	95.2	375	2	US-10-278-803-14
27	1906	95.2	375	2	US-09-841-730-2

28 1905 95.1 375 2 US-09-451-501-19 Sequence 19, Appl  
29 1905 95.1 375 2 US-10-278-803-19 Sequence 19, Appl  
30 1904 95.1 375 2 US-09-252-149B-30 Sequence 30, Appl  
31 1904 95.1 375 2 US-09-686-344-19 Sequence 19, Appl  
32 1904 95.1 375 2 US-09-626-896-10 Sequence 10, Appl  
33 1904 95.1 375 2 US-09-485-046-6 Sequence 6, Appl  
34 1904 95.1 375 2 US-09-841-730-10 Sequence 31, Appl  
35 1890 94.4 375 2 US-09-686-344-31 Sequence 16, Appl  
36 1890 94.4 375 2 US-09-626-896-16 Sequence 16, Appl  
37 1890 94.4 375 2 US-09-841-730-16 Sequence 33, Appl  
38 1887 94.2 375 2 US-09-252-149B-33 Sequence 12, Appl  
39 1876 93.7 376 1 US-08-525-596B-12 Sequence 12, Appl  
40 1876 93.7 376 2 US-09-177-860A-12 Sequence 6, Appl  
41 1876 93.7 376 2 US-08-891-789B-6 Sequence 27, Appl  
42 1876 93.7 376 2 US-09-252-149B-27 Sequence 12, Appl  
43 1876 93.7 376 2 US-09-378-238-12 Sequence 12, Appl  
44 1876 93.7 376 2 US-09-451-501-12 Sequence 12, Appl  
45 1876 93.7 376 2 US-09-629-938-12 Sequence 12, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-891-789B-2  
; Sequence 2, Application US/08891789B  
; Patent No. 6103466  
; GENERAL INFORMATION:  
; APPLICANT: Grobet, Luc; Georges, Michel  
; TITLE OF INVENTION: Double-Muscling in Mammals  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Blake, Cassels & Graydon  
; STREET: Box 25, Commerce Court West  
; CITY: Toronto  
; STATE: Ontario  
; ZIP: M5L 1A9  
; COUNTRY: Canada  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
; COMPUTER: COMPAQ, IBM PC compatible  
; OPERATING SYSTEM: MS-DOS 5.1  
; SOFTWARE: WORD PERFECT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/891.789B  
; FILING DATE: July 14, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunt, John C.  
; REGISTRATION NUMBER: 36,424  
; REFERENCE/DOCKET NUMBER: 52836/00004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 863-4344  
; TELEFAX: (416) 863-2653  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 375 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-891-789B-2

Query Match 100.0%; Score 2003; DB 2; Length 375;  
Best Local Similarity 100.0%; Pred. No. 1e-194;  
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MOKLQISVYIVFLMVLVAGPVDLNLNSENKGVKGLCNACLWRENTTSSRLRAIKQI 60  
Db 1 MOKLQISVYIVFLMVLVAGPVDLNLNSENKGVKGLCNACLWRENTTSSRLRAIKQI 60  
Qy 61 LSKRLLETAPNISKDAIRQLLPKAPPLLELDQFDVORDASSDGSLEDDDYHARTTIVIT 120  
Db 61 LSKRLLETAPNISKDAIRQLLPKAPPLLELDQFDVORDASSDGSLEDDDYHARTTIVIT 120

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds  
(without alignments)  
302.622 Million cell updates/sec

Title: US-09-628-112-10  
Perfect score: 2016  
Sequence: 1 MOKLQCVYIYFLMLVAGP.....KEQIIYKIPAMVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.New.\*  
1: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pap.\*  
2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pap.\*  
3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pap.\*  
4: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pap.\*  
5: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pap.\*  
6: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pap.\*  
7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pap.\*  
8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312.5	15.5	391	1	US-10-517-544-77
2	260	12.9	431	1	US-10-816-768-39
3	242.5	12.0	366	7	US-11-091-334-9
4	236.5	11.7	364	1	US-10-131-826A-342
5	236.5	11.7	364	7	US-11-091-334-2
6	234	11.6	429	1	US-10-967-457-74
7	232.5	11.5	102	1	US-10-816-768-47
8	225.5	11.2	102	1	US-10-816-768-53
9	223.5	11.1	129	1	US-10-816-768-89
10	223	11.1	139	1	US-10-816-768-68
11	222.5	11.0	203	1	US-10-816-768-100
12	221.5	11.0	102	1	US-10-816-768-46
13	221.5	11.0	117	1	US-10-816-768-69
14	216.5	10.7	102	1	US-10-816-768-85
15	216.5	10.7	102	1	US-10-816-768-86
16	214.5	10.6	102	1	US-10-816-768-84
17	213.5	10.6	102	1	US-10-816-768-88
18	213.5	10.6	102	1	US-10-816-768-88
19	212	10.5	101	1	US-10-816-768-59
20	208.5	10.3	106	1	US-10-816-768-62
21	208.5	10.3	106	1	US-10-816-768-63
22	207.5	10.3	102	1	US-10-816-768-52
23	207.5	10.3	102	1	US-10-816-768-56
24	206.5	10.2	102	1	US-10-816-768-87
25	206	10.2	101	1	US-10-816-768-49

26	205.5	10.2	102	1	US-10-816-768-83	Sequence 83, Appl
27	203.5	10.1	98	1	US-10-816-768-41	Sequence 41, Appl
28	203.5	10.1	98	1	US-10-816-768-42	Sequence 42, Appl
29	195	9.7	103	1	US-10-816-768-50	Sequence 50, Appl
30	194	9.6	101	1	US-10-816-768-51	Sequence 51, Appl
31	193.5	9.6	98	1	US-10-816-768-44	Sequence 44, Appl
32	192.5	9.5	98	1	US-10-816-768-43	Sequence 43, Appl
33	192.5	9.5	102	1	US-10-816-768-45	Sequence 45, Appl
34	189	9.4	107	1	US-10-816-768-58	Sequence 58, Appl
35	185.5	9.2	98	1	US-10-816-768-40	Sequence 40, Appl
36	182.5	9.1	98	1	US-10-816-768-64	Sequence 64, Appl
37	182	9.0	103	1	US-10-816-768-54	Sequence 54, Appl
38	178.5	8.9	118	1	US-10-816-768-48	Sequence 48, Appl
39	177.5	8.8	102	1	US-10-816-768-57	Sequence 57, Appl
40	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
41	146.5	7.3	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	113	5.6	105	1	US-10-816-768-61	Sequence 61, Appl
44	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
45	109	5.4	39	1	US-10-816-768-119	Sequence 119, App

ALIGNMENTS

RESULT 1  
US-10-517-544-77  
; Sequence 77, Application US/10517544  
; Publication No. US20050250100A1  
; GENERAL INFORMATION:  
; APPLICANT: RIKEN  
; APPLICANT: KABUSHIKI KAISHA DNAFORM  
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis  
; FILE REFERENCE: 1336(PCT)  
; CURRENT APPLICATION NUMBER: US/10/517,544  
; CURRENT FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: JP 2002-171851  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: JP 2002-235294  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 77  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-517-544-77

Query Match	15.5%	Score 312.5;	DB 1;	Length 391;
Best Local Similarity	27.2%	Pred. No. 3.3e-25;		
Matches	105;	Conservative 55;	Mismatches 131;	Indels 95; Gaps 15;
QY	49	KSRRTAKIKIQLSKRLTAPNISKDATRQLLPKAPPLRELIDQYDQVDDSDSDSLED	108	
DB	42	KKRIEARGIQLSKRLASPPSQS-----VPPGLPEAVLALYNSTRDVRAGSAEP	95	
QY	109	D-----DYHATTET-IITWPTESDPLMQVDPKPKCFKFSKIQNKVKVKAQLWLYL--	160	
DB	96	EPEPEADYAKETRVRLMVETHNEI-----YDKFKQSTHSIYMPF	135	
QY	161	-----RPVETPTTFVQILRLIKPMK-----DGTTRYTGIRSKLDNMPG	199	
DB	136	NTSELREAVPEPVLRLSLRAELRLRLKLVKEQHVLYQKYNNSWYLSNRLAPSDE	195	
QY	200	TGIMOSIDVKTVLQNLKQFESNLGIEIHA-----LDENGH-----DLAVTF	241	
DB	196	---WLSFDVTGVVROWLSRGEGIEGFRLSAHCSDSRDNTLQVDINGFTTGRGDLATI-	251	
QY	242	PGEGEDGLN-PIEVKVTDTPK-----RSRRDFGLDCDEHSTESRCRCRYPLTVDF-BA	292	
DB	252	-----HGMNRPPFLMLMATPLERAQHLQSSRRRALDNTYCFSTKCNCCVQRQYIYDFKD	306	
QY	293	LQWDWIIAPKRYKANYCSGCEBFVFLQKYPHTH---LVHQANPRGSAGPCCTPTKMSPIN	349	



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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds  
(without alignments)  
2359.729 Million cell updates/sec

Title: US-09-628-112-10

Perfect score: 2016

Sequence: 1 MOKLQLCVYILFVLMIVAGP.....KEQIIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2016	100.0	375	3	US-09-859-211-19
2	2016	100.0	375	3	US-09-841-730-10
3	2016	100.0	375	3	US-09-872-856-19
4	2016	100.0	375	4	US-10-074-152-30
5	2016	100.0	375	4	US-10-463-973-19
6	2016	100.0	375	4	US-10-456-852-6
7	2008	99.6	375	3	US-09-454-540-5
8	2008	99.6	375	3	US-09-859-211-14
9	2008	99.6	375	3	US-09-841-730-2
10	2008	99.6	375	3	US-09-872-856-14
11	2008	99.6	375	3	US-09-871-604-5
12	2008	99.6	375	4	US-10-074-152-29
13	2008	99.6	375	4	US-10-278-803-14
14	2008	99.6	375	4	US-10-071-499A-1
15	2008	99.6	375	4	US-10-335-483-14
16	2008	99.6	375	4	US-10-251-115-8
17	2008	99.6	375	4	US-10-253-532-130
18	2008	99.6	375	4	US-10-366-345-51
19	2008	99.6	375	4	US-10-463-973-14
20	2008	99.6	375	4	US-10-456-852-4
21	2008	99.6	375	4	US-10-459-127-5
22	2008	99.6	375	4	US-10-662-438-2
23	2008	99.6	375	5	US-10-689-677C-2
24	2008	99.6	375	5	US-10-665-374-2
25	2008	99.6	375	5	US-10-997-809-14
26	2008	99.6	375	5	US-10-991-343-14
27	2008	99.6	375	6	US-11-019-001-1

28	2008	99.6	376	3	US-09-813-398-38	Sequence 38, Appl
29	2008	99.6	376	5	US-10-826-324-38	Sequence 38, Appl
30	2007	99.6	375	4	US-10-278-803-19	Sequence 19, Appl
31	2003	99.4	375	3	US-09-859-894A-5	Sequence 5, Appl
32	1977	98.1	375	3	US-09-859-211-29	Sequence 29, Appl
33	1977	98.1	375	3	US-09-841-730-14	Sequence 14, Appl
34	1977	98.1	375	3	US-09-872-856-29	Sequence 29, Appl
35	1977	98.1	375	4	US-10-463-973-29	Sequence 29, Appl
36	1974	97.9	375	4	US-10-074-152-32	Sequence 32, Appl
37	1951	96.8	376	3	US-09-859-894A-11	Sequence 11, Appl
38	1951	96.8	376	3	US-09-859-211-12	Sequence 12, Appl
39	1951	96.8	376	3	US-09-841-730-4	Sequence 4, Appl
40	1951	96.8	376	3	US-09-872-856-12	Sequence 12, Appl
41	1951	96.8	376	3	US-09-871-604-10	Sequence 10, Appl
42	1951	96.8	376	4	US-10-074-152-27	Sequence 27, Appl
43	1951	96.8	376	4	US-10-278-803-12	Sequence 12, Appl
44	1951	96.8	376	4	US-10-335-483-12	Sequence 12, Appl
45	1951	96.8	376	4	US-10-251-115-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-09-859-211-19  
; Sequence 19, Application US/09859211  
; Patent No. US20020157125A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/859,211  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/019,070  
; PRIOR FILING DATE: 1998-02-05  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Baboon  
US-09-859-211-19

Query Match	100.0%;	Score	2016;	DB	3;	Length	375;
Best Local Similarity	100.0%;	Pred. No.	1.1e-182;				
Matches	375;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MOKLQLCVYILFVLMIVAGPVDLNNSEKENVKEGLCNACTWRQNTKSSRIEAIKIQI	60				
Db	1	MOKLQLCVYILFVLMIVAGPVDLNNSEKENVKEGLCNACTWRQNTKSSRIEAIKIQI	60				
Qy	61	LSKRLLETAPNISKDAIRQLLPKAPPLRELIDQDVQRDDSSDGSLEDDYHATTETIIT	120				
Db	61	LSKRLLETAPNISKDAIRQLLPKAPPLRELIDQDVQRDDSSDGSLEDDYHATTETIIT	120				
Qy	121	MPTESDFLMQVGDGPKCCFFKFSKIQYNKVVKQALMIYLPVETPTTVFVQILRLIKPM	180				
Db	121	MPTESDFLMQVGDGPKCCFFKFSKIQYNKVVKQALMIYLPVETPTTVFVQILRLIKPM	180				
Qy	181	KDGRYTGIRSLKLDMPNPGTGIWQSIDVKTVQLQNLKQPSNLGIEIKALDENGHLAVT	240				

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.39627 Seconds  
(without alignments)  
302.622 Million cell updates/sec

Title: US-09-628-112-8  
Perfect score: 2006  
Sequence: 1 QKLAVVYVILFMQIAVDPV.....KEQIIYGIKIPAMVVDRCGS 374

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB\_PEP.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB\_PEP.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB\_PEP.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB\_PEP.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB\_PEP.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB\_PEP.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB\_PEP.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315.5	15.7	391	1	US-10-517-544-77
2	255	12.7	431	1	US-10-816-768-39
3	237	11.8	429	1	US-10-967-457-74
4	235	11.7	364	1	US-10-131-826A-342
5	235	11.7	364	7	US-11-091-334-2
6	233.5	11.6	366	7	US-11-091-334-9
7	228.5	11.4	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.9	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.4	101	1	US-10-816-768-59
20	206.5	10.3	106	1	US-10-816-768-62
21	206.5	10.3	106	1	US-10-816-768-63
22	204	10.2	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

ALIGNMENTS

RESULT 1  
US-10-517-544-77  
; Sequence 77, Application US/10517544  
; Publication No. US20050250100A1  
; GENERAL INFORMATION:  
; APPLICANT: RIKEN  
; APPLICANT: KARUSHIKI KAISHA DNAFORM  
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis  
; FILE REFERENCE: 1336(PCT)  
; CURRENT APPLICATION NUMBER: US/10/517,544  
; CURRENT FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: JP 2002-171851  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: JP 2002-235294  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 77  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-517-544-77

Query Match	15.7%	Score 315.5;	DB 1;	Length 391;
Best Local Similarity	27.1%	Pred. No. 4.6e-25;		
Matches	105;	Conservative	57;	Mismatches 128;
				Indels 97;
				Gaps 16;
Qy	48	KSRIRIAIKTQILSKRLKLEQAPNISRVIKQLPKAPPLQELIDYQVQRDSDSGSLED	107	
Db	42	KRKRIEAIKQILSKRLASPPSQGE-----VPPGLPEAVLALYNSTRDRVAGESAEP	95	
Qy	108	D-----DYHATTET-IITMPTESEDFVQMEGPKCCFFKESKIQYNNKVAQLMIYL--	159	
Db	96	EPEPEADYAKETRVLMVETHNEI-----YDKFKQSTHSIYMPF	135	
Qy	160	-----RQVQKPTTVFVQILRLIKPMK-----DGTRYTGIRSLKLDMPG	198	
Db	136	NTSELREAVPEVPLUSRAELRLRLKLUKVEOHVELYQKYSNNRWYLNRLLPADSPE	195	
Qy	199	TGIMOSIDVKTVLQNLKQ-----PESNLGIEIKAFDETGR--DLAVT	239	
Db	196	---WLSFDVTGVVRQKLSRGGIEGFRLSAHCSDSDRNTLQVDINGP--TTGRGDLATI	251	
Qy	240	FPGPGEGLN--PFLEVRVTDTPK-----RSRRDFGLDCDDEHSTESRCRPLTVDFP-E	290	
Db	252	-----HGMNRPFLMLMATPLERAQHLQSSRRHRALDNYCFSSSTKNCVRLQYIDPRK	305	
Qy	291	AFGNDWIIAPKRYKANYCSGCEFFVLQKYPHTH---LVHQANPRGSAGPCCTPTTQMSPI	347	

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.2229 Seconds  
(without alignments)  
2359.729 Million cell updates/sec

Title: US-09-628-112-8

Perfect score: 206

Sequence: 1 OKLAVYVYIYLFMQIAVDPV.....KEQIIYKIPAMVDRGCS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	100.0	374	3	US-09-841-730-8
2	206	100.0	375	3	US-09-859-211-23
3	206	100.0	375	3	US-09-872-856-23
4	206	100.0	375	4	US-10-463-973-23
5	206	100.0	375	4	US-10-456-852-10
6	206	100.0	375	4	US-10-662-438-6
7	206	100.0	375	5	US-10-665-374-6
8	2003	99.9	375	4	US-10-074-152-34
9	1989	99.2	375	3	US-09-859-211-27
10	1989	99.2	375	3	US-09-841-730-18
11	1989	99.2	375	3	US-09-872-856-27
12	1989	99.2	375	4	US-10-463-973-27
13	1989	99.2	375	4	US-10-456-852-14
14	1978	98.6	375	4	US-10-074-152-35
15	1976	98.5	375	4	US-10-278-803-23
16	1959	97.7	375	4	US-10-278-803-27
17	1860	92.7	375	3	US-09-454-540-5
18	1860	92.7	375	3	US-09-859-211-14
19	1860	92.7	375	3	US-09-841-730-2
20	1860	92.7	375	3	US-09-872-856-14
21	1860	92.7	375	3	US-09-871-604-5
22	1860	92.7	375	4	US-10-074-152-29
23	1860	92.7	375	4	US-10-278-803-14
24	1860	92.7	375	4	US-10-071-499A-1
25	1860	92.7	375	4	US-10-335-483-14
26	1860	92.7	375	4	US-10-251-115-8
27	1860	92.7	375	4	US-10-253-532-130

28	1860	92.7	375	4	US-10-366-345-51	Sequence 51, Appl
29	1860	92.7	375	4	US-10-463-973-14	Sequence 14, Appl
30	1860	92.7	375	4	US-10-456-852-4	Sequence 4, Appl
31	1860	92.7	375	4	US-10-459-127-5	Sequence 5, Appl
32	1860	92.7	375	4	US-10-662-438-2	Sequence 2, Appl
33	1860	92.7	375	5	US-10-688-677C-2	Sequence 2, Appl
34	1860	92.7	375	5	US-10-665-374-2	Sequence 2, Appl
35	1860	92.7	375	5	US-10-997-809-14	Sequence 14, Appl
36	1860	92.7	375	5	US-10-991-343-14	Sequence 14, Appl
37	1860	92.7	375	6	US-11-019-001-1	Sequence 1, Appl
38	1860	92.7	376	3	US-09-813-398-38	Sequence 38, Appl
39	1860	92.7	376	5	US-10-826-324-38	Sequence 38, Appl
40	1855	92.5	375	3	US-09-859-894A-5	Sequence 5, Appl
41	1855	92.5	375	3	US-09-859-211-29	Sequence 29, Appl
42	1855	92.5	375	3	US-09-841-730-14	Sequence 14, Appl
43	1855	92.5	375	3	US-09-872-856-29	Sequence 29, Appl
44	1855	92.5	375	4	US-10-463-973-29	Sequence 29, Appl
45	1852	92.3	375	4	US-10-074-152-32	Sequence 32, Appl

#### ALIGNMENTS

RESULT 1  
US-09-841-730-8  
; Sequence 8, Application US/09841730  
; Patent No. US20020157126A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,  
; FILE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME  
; FILE REFERENCE: JHU1470-2  
; CURRENT APPLICATION NUMBER: US/09/841,730  
; CURRENT FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: 09/626,896  
; PRIOR FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 09/485,046  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: PCT/US98/155598  
; PRIOR FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: 60/054,461  
; PRIOR FILING DATE: 1997-08-01  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-841-730-8

Query Match 100.0%; Score 2066; DB 3; Length 374;  
Best Local Similarity 100.0%; Pred. No. 1.3e-180;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	OKLAVYVYIYLFMQIAVDPVALDGSSQPTENAEKGLCNACTWRONTKSSRIEAIKQIL	60
Db	1	OKLAVYVYIYLFMQIAVDPVALDGSSQPTENAEKGLCNACTWRONTKSSRIEAIKQIL	60
Qy	61	SKLLEQAPNISRDVIKQLLPKAPPLQELIDQYDVQDRDSDGSLDDDDYHATTETITM	120
Db	61	SKLLEQAPNISRDVIKQLLPKAPPLQELIDQYDVQDRDSDGSLDDDDYHATTETITM	120
Qy	121	PTESDFLVOMEKPKCCFFKPSKIQNVKVAQIWIYLRQVOKPTTVFVQILRLIKPMK	180
Db	121	PTESDFLVOMEKPKCCFFKPSKIQNVKVAQIWIYLRQVOKPTTVFVQILRLIKPMK	180
Qy	181	DGRTYTGIRSLKLDNPGTGIWQSIDVKTVLQNLKQPESNLGIEIKAFDETGRDLAVTF	240
Db	181	DGRTYTGIRSLKLDNPGTGIWQSIDVKTVLQNLKQPESNLGIEIKAFDETGRDLAVTF	240
Qy	241	PGPGEDGLNPFLEVRVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIAP	300
Db	241	PGPGEDGLNPFLEVRVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIAP	300

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.2512 Seconds  
(without alignments)  
1694.174 Million cell updates/sec

Title: US-09-628-112-8

Perfect score: 2006

Sequence: 1 QKLVVYVYLFMQIAVDPV.....KEQIIVGKIPAMVVDRCGS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/PCUS COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2006	100.0	374	2	US-09-626-896-8
2	2006	100.0	374	2	US-09-841-730-8
3	2006	100.0	375	2	US-09-686-344-23
4	2006	100.0	375	2	US-09-485-046-10
5	2003	99.9	375	2	US-09-252-149B-34
6	1989	99.2	375	2	US-09-686-344-27
7	1989	99.2	375	2	US-09-626-896-18
8	1989	99.2	375	2	US-09-485-046-14
9	1989	99.2	375	2	US-09-841-730-18
10	1978	98.6	375	2	US-09-252-149B-35
11	1976	98.5	375	2	US-09-451-501-23
12	1976	98.5	375	2	US-10-278-803-23
13	1959	97.7	375	2	US-09-451-501-27
14	1959	97.7	375	2	US-10-278-803-27
15	1860	92.7	375	1	US-08-525-596B-14
16	1860	92.7	375	1	US-08-765-875-5
17	1860	92.7	375	2	US-08-795-671-5
18	1860	92.7	375	2	US-09-177-860A-14
19	1860	92.7	375	2	US-09-252-149B-29
20	1860	92.7	375	2	US-09-378-238-14
21	1860	92.7	375	2	US-09-451-501-14
22	1860	92.7	375	2	US-09-629-938-14
23	1860	92.7	375	2	US-09-454-540-5
24	1860	92.7	375	2	US-09-626-344-14
25	1860	92.7	375	2	US-09-485-046-4
26	1860	92.7	375	2	US-09-485-046-4
27	1860	92.7	375	2	US-10-278-803-14

28	1860	92.7	375	2	US-09-841-730-2	Sequence 2, Appli
29	1855	92.5	375	2	US-09-686-344-29	Sequence 29, Appli
30	1855	92.5	375	2	US-09-626-896-14	Sequence 14, Appli
31	1855	92.5	375	2	US-09-841-730-14	Sequence 14, Appli
32	1852	92.3	375	2	US-09-252-149B-32	Sequence 32, Appli
33	1851	92.3	375	2	US-09-451-501-19	Sequence 19, Appli
34	1851	92.3	375	2	US-10-278-803-19	Sequence 19, Appli
35	1850	92.2	375	2	US-09-252-149B-30	Sequence 30, Appli
36	1850	92.2	375	2	US-09-686-344-19	Sequence 19, Appli
37	1850	92.2	375	2	US-09-626-896-10	Sequence 10, Appli
38	1850	92.2	375	2	US-09-485-046-6	Sequence 6, Appli
39	1850	92.2	375	2	US-09-841-730-10	Sequence 10, Appli
40	1842	91.8	376	1	US-08-525-596B-12	Sequence 12, Appli
41	1842	91.8	376	2	US-09-177-860A-12	Sequence 12, Appli
42	1842	91.8	376	2	US-08-891-789B-6	Sequence 6, Appli
43	1842	91.8	376	2	US-09-252-149B-27	Sequence 27, Appli
44	1842	91.8	376	2	US-09-378-238-12	Sequence 12, Appli
45	1842	91.8	376	2	US-09-451-501-12	Sequence 12, Appli

## ALIGNMENTS

RESULT 1

US-09-626-896-8

/ Sequence 8, Application US/09626896

/ Patent No. 6656475

/ GENERAL INFORMATION:

/ APPLICANT: Lee, Se-Jin

/ APPLICANT: McPherron, Alexandra C.

/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,

/ AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME

/ FILE REFERENCE: JHU1470-2

/ CURRENT APPLICATION NUMBER: US/09/626,896

/ CURRENT FILING DATE: 2000-07-27

/ PRIOR APPLICATION NUMBER: 09/485,046

/ PRIOR FILING DATE: 2000-01-31

/ PRIOR APPLICATION NUMBER: PCT/US98/15598

/ PRIOR FILING DATE: 1998-07-28

/ PRIOR APPLICATION NUMBER: 60/054,461

/ PRIOR FILING DATE: 1997-08-01

/ NUMBER OF SEQ ID NOS: 29

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 8

/ LENGTH: 374

/ TYPE: PRT

/ ORGANISM: Gallus gallus

US-09-626-896-8

Query Match

Best Local Similarity 100.0%; Score 2006; DB 2; Length 374;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKLVVYVYLFMQIAVDPVALDGSQPTENAEDGLNACTWONTKSSRIEAIKQIL 60

Db 1 QKLVVYVYLFMQIAVDPVALDGSQPTENAEDGLNACTWONTKSSRIEAIKQIL 60

QY 61 SKLRLEQAPNISRDVIKQLLPKAPLOQLIDQYDQVDRDSSDGSLEDDDYHATTETIIM 120

Db 61 SKLRLEQAPNISRDVIKQLLPKAPLOQLIDQYDQVDRDSSDGSLEDDDYHATTETIIM 120

QY 121 PTESDFLVQMEGKPKCCFFKPFSSKIYKNVKAQIWLVRQVKPTTVFVQLIRLKPWK 180

Db 121 PTESDFLVQMEGKPKCCFFKPFSSKIYKNVKAQIWLVRQVKPTTVFVQLIRLKPWK 180

QY 181 DGYRTYGIKSLDMNPCTGHWQSIDVKTVLQNLKQPSNLGIEIKAFDETRDLAVTF 240

Db 181 DGYRTYGIKSLDMNPCTGHWQSIDVKTVLQNLKQPSNLGIEIKAFDETRDLAVTF 240

QY 241 PGPGEGLNPPLEVRVTDTPKSRREDGLDCDEHSTSRCCRYPLTVDFEAFGWDWIAP 300

Db 241 PGPGEGLNPPLEVRVTDTPKSRREDGLDCDEHSTSRCCRYPLTVDFEAFGWDWIAP 300

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.40373 Seconds  
(without alignments)  
302.622 Million cell updates/sec

Title: US-09-628-112-6  
Perfect score: 2019  
Sequence: 1 MTKQPMYVYVLFVLIAG.....KEQIYKIPAMVDRGCS 376

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : 1: /cgn2\_6/prodata/1/pubaa/US10\_NEW\_PUB pep.\*  
2: /cgn2\_6/prodata/1/pubaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/prodata/1/pubaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/prodata/1/pubaa/US08\_NEW\_PUB pep.\*  
5: /cgn2\_6/prodata/1/pubaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/prodata/1/pubaa/PCT\_NEW\_PUB pep.\*  
7: /cgn2\_6/prodata/1/pubaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/prodata/1/pubaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	311.5	15.4	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	242	12.0	366	7	US-11-091-334-9
4	236	11.7	429	1	US-10-967-457-74
5	232	11.5	364	1	US-10-131-826A-342
6	232	11.5	364	7	US-11-091-334-2
7	228.5	11.3	102	1	US-10-816-768-47
8	221.5	10.9	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.8	139	1	US-10-816-768-68
12	218.5	10.8	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.5	102	1	US-10-816-768-85
15	212.5	10.5	102	1	US-10-816-768-86
16	210.5	10.4	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.2	106	1	US-10-816-768-62
21	206.5	10.2	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.0	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.6	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.4	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.3	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.8	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.6	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.1	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

## ALIGNMENTS

RESULT 1  
US-10-517-544-77  
; Sequence 77, Application US/10517544  
; Publication NO. US20050250100A1  
; GENERAL INFORMATION:  
; APPLICANT: RIKEN  
; APPLICANT: KABUSHIKI KAISHA DNAFORM  
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis  
; FILE REFERENCE: 1336 (PCT)  
; CURRENT APPLICATION NUMBER: US/10/517,544  
; CURRENT FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: JP 2002-171851  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: JP 2002-235294  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 77  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-517-544-77

Query Match	15.4%	Score 311.5;	DB 1;	Length 391;
Best Local Similarity	27.4%	Pred. No. 1.2e-24;		
Matches	105;	Conservative	54;	Mismatches 129; Indels 95; Gaps 15;
QY	53	RIEAIKIQILSKLRLETAFNISKDAIRQLPRAPPRELIDQYDVQDSSDGSLED--	110	
DB	45	RIEAIQILSKLRLASPPSQGE-----VPGPLPEAVLALYNSTRDVAGESASPEPE	98	
QY	111	---DYHATTET-IITMPTESDFLMQDQPKCFKFFSKIQNKVKVKAQLWLYL----	161	
DB	99	PEADYYAKEVTRVLMVETHNEI-----YDFKQKSTHMYFNTS	138	
QY	162	---RAVKTPPTTVFQVQLRLIKPMK-----DGTRYTGIRSLKLDMSPTGTI	203	
DB	139	EUREAVPEPVLUSRAELRLRLRLKUKVEQHVLYQKYSNNRWYLSNRLAPSDSPE---	195	
QY	204	WQSIDVKTVLQNLKOPESNLGIEIKA-----LDENGH-----DLAVTFPGP	245	
DB	196	WLSFDVTGVVRQWLSRGGEIEGFRLSAHCSDSRDNTLQVDINGFTTGRGDLATI----	251	
QY	246	GSDGLN-PPELVKVTUTPK-----RSRRDFGLDCDEHSTESRCRCRYLTVDF-BAFGW	296	
DB	252	--HGMNRPFLMLMATPLERAQHLQSSRRRALDNTYCFSSSTKNCVQVLYIDFRKDLGW	309	
QY	297	DWIIAPKRYKANYCSGECEVFVLOQYPHTH---LVHQANPRGSAGPCCTPTKMSPINMLY	353	

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 22, 2005, 17:13:27 ; Search time 66.5771 Seconds  
(without-alignments)  
2359.729 Million cell updates/sec

Title: US-09-628-112-6  
Perfect score: 2019  
Sequence: 1 MIQKPMYIYLVFLIAG.....KEIYIKIPAMVDRCCS 376  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues  
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:  
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4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pap.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2019	100.0	376	3	US-09-859-211-25 Sequence 25, Appl
2	2019	100.0	376	3	US-09-841-730-6 Sequence 6, Appl
3	2019	100.0	376	3	US-09-872-856-25 Sequence 25, Appl
4	2019	100.0	376	4	US-10-074-152-28 Sequence 28, Appl
5	2019	100.0	376	4	US-10-278-803-25 Sequence 25, Appl
6	2019	100.0	376	4	US-10-463-973-25 Sequence 25, Appl
7	2019	100.0	376	4	US-10-456-852-12 Sequence 12, Appl
8	1986	98.4	376	3	US-09-859-894A-11 Sequence 11, Appl
9	1986	98.4	376	3	US-09-859-211-12 Sequence 12, Appl
10	1986	98.4	376	3	US-09-841-730-4 Sequence 4, Appl
11	1986	98.4	376	3	US-09-872-856-12 Sequence 12, Appl
12	1986	98.4	376	3	US-09-871-604-10 Sequence 10, Appl
13	1986	98.4	376	4	US-10-074-152-27 Sequence 27, Appl
14	1986	98.4	376	4	US-10-278-803-12 Sequence 12, Appl
15	1986	98.4	376	4	US-10-335-483-12 Sequence 12, Appl
16	1986	98.4	376	4	US-10-251-115-6 Sequence 6, Appl
17	1986	98.4	376	4	US-10-463-973-12 Sequence 12, Appl
18	1986	98.4	376	4	US-10-456-852-2 Sequence 2, Appl
19	1986	98.4	376	4	US-10-459-127-10 Sequence 10, Appl
20	1986	98.4	376	4	US-10-997-809-12 Sequence 12, Appl
21	1986	98.4	376	5	US-10-991-343-12 Sequence 12, Appl
22	1932	95.7	375	4	US-10-278-803-19 Sequence 19, Appl
23	1931	95.6	375	3	US-10-074-152-32 Sequence 32, Appl
24	1928	95.5	375	3	US-09-859-211-29 Sequence 29, Appl
25	1928	95.5	375	3	US-09-841-730-14 Sequence 14, Appl
26	1928	95.5	375	3	US-09-872-856-29 Sequence 29, Appl
27	1928	95.5	375	4	US-10-463-973-29 Sequence 29, Appl

28	1925	95.3	375	3	US-09-454-540-5 Sequence 5, Appl
29	1925	95.3	375	3	US-09-859-211-14 Sequence 14, Appl
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31	1925	95.3	375	3	US-09-872-856-14 Sequence 14, Appl
32	1925	95.3	375	3	US-09-871-604-5 Sequence 5, Appl
33	1925	95.3	375	4	US-10-074-152-29 Sequence 29, Appl
34	1925	95.3	375	4	US-10-278-803-14 Sequence 14, Appl
35	1925	95.3	375	4	US-10-071-499A-1 Sequence 1, Appl
36	1925	95.3	375	4	US-10-335-483-14 Sequence 14, Appl
37	1925	95.3	375	4	US-10-251-115-8 Sequence 8, Appl
38	1925	95.3	375	4	US-10-253-532-130 Sequence 130, Appl
39	1925	95.3	375	4	US-10-366-345-51 Sequence 51, Appl
40	1925	95.3	375	4	US-10-463-973-14 Sequence 14, Appl
41	1925	95.3	375	4	US-10-456-852-4 Sequence 4, Appl
42	1925	95.3	375	4	US-10-459-137-5 Sequence 5, Appl
43	1925	95.3	375	4	US-10-662-438-2 Sequence 2, Appl
44	1925	95.3	375	5	US-10-689-677C-2 Sequence 2, Appl
45	1925	95.3	375	5	US-10-665-374-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1  
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; Sequence 25, Application US/09859211  
; Patent No. US20020157125A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; FILE REFERENCE: 07265/144001  
; CURRENT APPLICATION NUMBER: US/09/859,211  
; CURRENT FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 09/019,070  
; PRIOR FILING DATE: 1998-02-05  
; PRIOR APPLICATION NUMBER: 08/862,445  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 08/847,910  
; PRIOR FILING DATE: 1997-04-28  
; PRIOR APPLICATION NUMBER: 08/795,071  
; PRIOR FILING DATE: 1997-02-05  
; PRIOR APPLICATION NUMBER: 08/525,596  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: PCT/US94/03019  
; PRIOR FILING DATE: 1994-03-18  
; PRIOR APPLICATION NUMBER: 08/033,923  
; PRIOR FILING DATE: 1993-03-19  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-859-211-25

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Matches 376;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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DB	1	MIQKPMYIYLVFLIAGPVDLNE	SREANVEKEGLCNACAWQNT	YSRIBAIKIQ	60
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QY	181	MKDGTRYTGIRSLKLDMSFGT	GIWQSIDVKTVLQNLWKQPE	SNIGIEIKALDENGHLAV	240

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3488 Seconds  
(without alignments)  
1694.174 Million cell updates/sec

Title: US-09-628-112-4

Perfect score: 2022

Sequence: 1 MMQKLMYYIYLFMLIAG.....KEQIYGIKIPAMVDRCGS 376

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2022	100.0	376	2	US-08-991-789B-6
4	2022	100.0	376	2	US-09-252-149B-27
5	2022	100.0	376	2	US-09-378-238-12
6	2022	100.0	376	2	US-09-451-501-12
7	2022	100.0	376	2	US-09-629-938-12
8	2022	100.0	376	2	US-09-686-344-12
9	2022	100.0	376	2	US-09-626-896-4
10	2022	100.0	376	2	US-09-485-046-2
11	2022	100.0	376	2	US-10-278-803-12
12	2022	100.0	376	2	US-09-841-730-4
13	1986	98.2	376	2	US-09-252-149B-28
14	1986	98.2	376	2	US-09-451-501-25
15	1986	98.2	376	2	US-09-686-344-25
16	1986	98.2	376	2	US-09-626-896-6
17	1986	98.2	376	2	US-09-485-046-12
18	1986	98.2	376	2	US-10-278-803-25
19	1986	98.2	376	2	US-09-841-730-6
20	1960	96.9	375	2	US-09-451-501-19
21	1960	96.9	375	2	US-10-278-803-19
22	1959	96.9	375	2	US-09-252-149B-32
23	1956	96.7	375	2	US-09-686-344-29
24	1956	96.7	375	2	US-09-626-896-14
25	1956	96.7	375	2	US-09-841-730-14
26	1953	96.6	375	1	US-08-525-596B-14
27	1953	96.6	375	1	US-08-765-875-5

28	1953	96.6	375	2	US-08-795-671-5	Sequence 5, Appl
29	1953	96.6	375	2	US-09-177-860A-14	Sequence 14, Appl
30	1953	96.6	375	2	US-09-252-149B-29	Sequence 29, Appl
31	1953	96.6	375	2	US-09-378-238-14	Sequence 14, Appl
32	1953	96.6	375	2	US-09-451-501-14	Sequence 14, Appl
33	1953	96.6	375	2	US-09-629-938-14	Sequence 14, Appl
34	1953	96.6	375	2	US-09-454-540-5	Sequence 5, Appl
35	1953	96.6	375	2	US-09-686-344-14	Sequence 14, Appl
36	1953	96.6	375	2	US-09-626-896-2	Sequence 2, Appl
37	1953	96.6	375	2	US-09-485-046-4	Sequence 4, Appl
38	1953	96.6	375	2	US-10-278-803-14	Sequence 14, Appl
39	1953	96.6	375	2	US-09-841-730-2	Sequence 2, Appl
40	1951	96.5	375	2	US-09-252-149B-30	Sequence 30, Appl
41	1951	96.5	375	2	US-09-686-344-19	Sequence 19, Appl
42	1951	96.5	375	2	US-09-626-896-10	Sequence 10, Appl
43	1951	96.5	375	2	US-09-485-046-6	Sequence 6, Appl
44	1951	96.5	375	2	US-09-841-730-10	Sequence 10, Appl
45	1953	93.6	375	2	US-09-252-149B-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1  
US-08-525-596B-12  
; Sequence 12, Application US/08525596B  
; Patent No. 5827733  
; GENERAL INFORMATION:  
; APPLICANT: Huynh, Thanh  
; APPLICANT: Lee, Se-Jin  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/525,596B  
; FILING DATE: 19-SEP-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07762  
; FILING DATE: 08-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wetherell, Jr., Ph.D, John R.  
; REGISTRATION NUMBER: 31,678  
; REFERENCE/DOCKET NUMBER: 07265/075001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-678-5070  
; TELEFAX: 619-678-5099  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 376 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-525-596B-12

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Best Local Similarity 100.0%; Pred. No. 7.9e-197;  
Matches 376; Conservative 0; Mismatches 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.5771 Seconds  
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2359.729 Million cell updates/sec

Title: US-09-628-112-4  
Perfect score: 2022  
Sequence: 1 MMQKLMVYIYLFMLIAAG.....KEQIIYKIPAMVDRCGCS 376

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/prodata/1/pubpaa/US10\_PUBCOMB.pap:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2022	100.0	376	3 US-09-859-894A-11	Sequence 11, Appl
2	2022	100.0	376	3 US-09-859-211-12	Sequence 12, Appl
3	2022	100.0	376	3 US-09-841-730-4	Sequence 4, Appl
4	2022	100.0	376	3 US-09-872-856-12	Sequence 12, Appl
5	2022	100.0	376	3 US-09-871-604-10	Sequence 10, Appl
6	2022	100.0	376	4 US-10-074-152-27	Sequence 27, Appl
7	2022	100.0	376	4 US-10-278-803-12	Sequence 12, Appl
8	2022	100.0	376	4 US-10-335-483-12	Sequence 12, Appl
9	2022	100.0	376	4 US-10-251-115-6	Sequence 6, Appl
10	2022	100.0	376	4 US-10-463-973-12	Sequence 12, Appl
11	2022	100.0	376	4 US-10-456-852-2	Sequence 2, Appl
12	2022	100.0	376	4 US-10-459-127-10	Sequence 10, Appl
13	2022	100.0	376	5 US-10-997-809-12	Sequence 12, Appl
14	2022	100.0	376	5 US-10-991-343-12	Sequence 12, Appl
15	1986	98.2	376	3 US-09-859-211-25	Sequence 25, Appl
16	1986	98.2	376	3 US-09-841-730-6	Sequence 6, Appl
17	1986	98.2	376	3 US-09-872-856-25	Sequence 25, Appl
18	1986	98.2	376	4 US-10-074-152-28	Sequence 28, Appl
19	1986	98.2	376	4 US-10-278-803-25	Sequence 25, Appl
20	1986	98.2	376	4 US-10-463-973-25	Sequence 25, Appl
21	1986	98.2	376	4 US-10-456-852-12	Sequence 12, Appl
22	1960	96.9	375	4 US-10-278-803-19	Sequence 19, Appl
23	1959	96.9	375	4 US-10-074-152-32	Sequence 32, Appl
24	1956	96.7	375	3 US-09-859-211-29	Sequence 29, Appl
25	1956	96.7	375	3 US-09-841-730-14	Sequence 14, Appl
26	1956	96.7	375	3 US-09-872-856-29	Sequence 29, Appl
27	1956	96.7	375	4 US-10-463-973-29	Sequence 29, Appl

28	1953	96.6	375	3 US-09-454-540-5	Sequence 5, Appl
29	1953	96.6	375	3 US-09-859-211-14	Sequence 14, Appl
30	1953	96.6	375	3 US-09-841-730-2	Sequence 2, Appl
31	1953	96.6	375	3 US-09-872-856-14	Sequence 14, Appl
32	1953	96.6	375	3 US-09-871-604-5	Sequence 5, Appl
33	1953	96.6	375	4 US-10-074-152-29	Sequence 29, Appl
34	1953	96.6	375	4 US-10-278-803-14	Sequence 14, Appl
35	1953	96.6	375	4 US-10-071-499A-1	Sequence 1, Appl
36	1953	96.6	375	4 US-10-335-483-14	Sequence 14, Appl
37	1953	96.6	375	4 US-10-251-115-8	Sequence 8, Appl
38	1953	96.6	375	4 US-10-253-532-130	Sequence 130, Appl
39	1953	96.6	375	4 US-10-366-345-51	Sequence 51, Appl
40	1953	96.6	375	4 US-10-463-973-14	Sequence 14, Appl
41	1953	96.6	375	4 US-10-456-852-4	Sequence 4, Appl
42	1953	96.6	375	4 US-10-459-127-5	Sequence 5, Appl
43	1953	96.6	375	4 US-10-662-438-2	Sequence 2, Appl
44	1953	96.6	375	5 US-10-689-677C-2	Sequence 2, Appl
45	1953	96.6	375	5 US-10-665-374-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-859-894A-11  
; Sequence 11, Application US/09859894A  
; Patent No. US20020150577A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: Lee, Se-Jin  
; APPLICANT: McPherron, Alexandra C.  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11  
; FILE REFERENCE: JHU1200-9  
; CURRENT APPLICATION NUMBER: US/09/859,894A  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/019,901  
; PRIOR FILING DATE: 1998-02-06  
; PRIOR APPLICATION NUMBER: 08/795,671  
; PRIOR FILING DATE: 1997-02-06  
; PRIOR APPLICATION NUMBER: 08/706,958  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/272,763  
; PRIOR FILING DATE: 1994-07-08  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-859-894A-11

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				Indels	0;
				Gaps	0;
Qy	1	MMQKLMVYIYLFMLIAAGPVDLNEGSEENVEKGLCNACAWQNTYRSIEAIKIQ	60		
Db	1	MMQKLMVYIYLFMLIAAGPVDLNEGSEENVEKGLCNACAWQNTYRSIEAIKIQ	60		
Qy	61	ILSKLLETAPNISKDAIRQLPRAPRLIDQYDQVDRDSDSGSLEDDDYHATTETII	120		
Db	61	ILSKLLETAPNISKDAIRQLPRAPRLIDQYDQVDRDSDSGSLEDDDYHATTETII	120		
Qy	121	TMPTESDFLMAQDGKPKCCFFKSSKIYQNVKVAQLWIYLRPVKTPPTTVFVQILRLIKP	180		
Db	121	TMPTESDFLMAQDGKPKCCFFKSSKIYQNVKVAQLWIYLRPVKTPPTTVFVQILRLIKP	180		
Qy	181	MKDGTTRYTGIRSLKLDMSPGTGIWQSIDVKTIVLQNLKQPESNLGIBIKALDENGHLAV	240		
Db	181	MKDGTTRYTGIRSLKLDMSPGTGIWQSIDVKTIVLQNLKQPESNLGIBIKALDENGHLAV	240		
Qy	241	TFPGPESDGLNPFLVKKVTTTPKGRRRDFGLDCDEHSTESRCRYPLTVDPFGAWDII	300		



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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.40373 Seconds  
(without alignments)  
302.622 Million cell updates/sec

Title: US-09-628-112-4  
Perfect score: 2022  
Sequence: 1 MMQKLMYVYVLFMLIAAG.....KEQIYKIPAMVVDRCGS 376

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
1: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB pep.\*  
2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB pep.\*  
5: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB pep.\*  
7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	306.5	15.2	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	249	12.3	366	7	US-11-091-334-9
4	236	11.7	429	1	US-10-967-457-74
5	232	11.5	364	1	US-10-131-826A-342
6	232	11.5	364	7	US-11-091-334-2
7	228.5	11.3	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.8	139	1	US-10-816-768-88
12	218.5	10.8	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.5	102	1	US-10-816-768-85
15	212.5	10.5	102	1	US-10-816-768-86
16	210.5	10.4	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.2	106	1	US-10-816-768-62
21	206.5	10.2	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.0	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.5	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.4	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.3	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.2	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.8	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.6	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.0	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1  
US-10-517-544-77  
; Sequence 77, Application US/10517544  
; Publication No. US20050250100A1  
; GENERAL INFORMATION:  
; APPLICANT: RIKEN  
; APPLICANT: KABUSHIKI KAISHA DNAFORM  
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis  
; FILE REFERENCE: 1336(PCT)  
; CURRENT APPLICATION NUMBER: US/10/517,544  
; PRIOR FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: JP 2002-171851  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: JP 2002-235294  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 77  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-517-544-77

Query Match	15.2%	Score 306.5;	DB 1;	Length 391;
Best Local Similarity	28.1%	Pred. No. 3.1e-24;		
Matches 103;	Conservative 56;	Mismatches 146;	Indels 61;	Gaps 14;
QY	53	R E A I K I Q I L S K L R L E T A P N I S K D A I R Q L L P R A P P L R E L I D Q Y D V O R D S S D G S L E D D --	110	
Db	45	R I E A R G Q I L S K L R L A S P P S Q G E ----- V P G P L P E A V L A L Y N S T R D R V A G S A E P E	98	
QY	111	--- D V H A T T I T I M P T E S D F L M Q A D G K P C C F K S S K I O N K V V ----- K A O L W I Y	160	
Db	99	P R A D Y A K E V T R V L M V M T H E N E I Y D K F Q S T H S I Y M F N T S E L R E A V P E P V L L S R A E L R L --	157	
QY	161	L R P V K T P T T V F Q I L R L I K P M K D G T R Y T G I R S I K L D M S P G T G I W Q S I D V K T V L Q N L M K Q P	220	
Db	158	L R R L K L V Q H V E L Y Q -- K Y S N N S W Y L S N R L L A P S D S P E --- W L S F D V T G V V R Q M L S R G	212	
QY	221	E S N L G I E I K A ----- L D E N G H ----- D L A V T F P G C E D G L N - P F L E V K V T D T	261	
Db	213	G E I G F R L S A H C S C S D R N T L Q V D I N G F T T G R R G D L A T I ----- H G M N R P F L L M A T P L	266	
QY	262	P K ----- R S R D F G L D C D E H S T E S R C C R Y P L T V D F - E A F G W D W I I A P K R Y A N Y C S G E	313	
Db	267	E R A Q H L Q S R H R A L D T N Y C F S T E K N C C V R Q L Y I D F R K D L G M K W I H E P R G Y H A N F C L G P	326	
QY	314	C E F V F L Q K Y P H T H --- L V H Q A N P R G S A G P C C T P T K M S P I N M L Y F N G K E Q I I Y K I P A M V V	370	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds  
(without alignments)  
302.622 Million cell updates/sec

Title: US-09-628-112-2

Perfect score: 2018

Sequence: 1 MQLQLCVYILFMLIVAGP.....KEQLIYKIPAMVDRCGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.\*

- 1: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pbp.\*
- 2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pbp.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pbp.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pbp.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pbp.\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pbp.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pbp.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pbp.\*

Pred. No. is the number of results predicted by chance to have a  
... score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	308.5	15.3	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	238.5	11.8	366	7	US-11-091-334-9
4	232	11.5	364	1	US-10-131-826A-342
5	232	11.5	364	7	US-11-091-334-2
6	231	11.4	429	1	US-10-967-457-74
7	228.5	11.3	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.8	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.5	102	1	US-10-816-768-85
15	212.5	10.5	102	1	US-10-816-768-86
16	210.5	10.4	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.2	106	1	US-10-816-768-62
21	206.5	10.2	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.0	102	1	US-10-816-768-87	Sequence 87, Appl
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32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.3	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.8	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.6	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.1	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

#### ALIGNMENTS

RESULT 1  
US-10-517-544-77  
; Sequence 77, Application US/10517544  
; Publication No. US20050250100A1  
; GENERAL INFORMATION:  
; APPLICANT: RIKEN  
; APPLICANT: KABUSHIKI KAISHA DNAFORM  
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis  
; FILE REFERENCE: 1336(PCT)  
; CURRENT APPLICATION NUMBER: US/10/517,544  
; PRIOR FILING DATE: 2004-12-10  
; PRIOR APPLICATION NUMBER: JP 2002-171851  
; PRIOR FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: JP 2002-235294  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 77  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-517-544-77

Query Match	15.3%;	Score 308.5;	DB 1;	Length 391;
Best Local Similarity	26.9%;	Pred. No. 1.7e-24;		
Matches 104;	Conservative 55;	Mismatches 132;	Indels 95;	Gaps 15;
QY	49	KSRIRIARIQILSKRLTAPNISKDVIRQLLPKAPPLRELDIQVDVQRDDSDGSLD	108	
Db	42	KRKRIEIRGQILSKRLASPPSQGE-----VPPGPLPEAVLALYNSTRDRVAGESABP	95	
QY	109	D-----DYATATET-IITPTESDPLMQVDGPKCFKPFSSKIQYKVKVKAQIMYL--	160	
Db	96	EPEPEADYYAKETRVLMVETHEI-----YDKFKQSTHSITWFF	135	
QY	161	-----RPVETPTTVFQILRLIKPMK-----DGTRYTGIRSLKLDNPNP	199	
Db	136	NTSELREANPEFVLLSRARLRLRLKLVQHVLYQKYSNNRWLSNLLAPSDSPE	195	
QY	200	TGIWQSIDVKTVLQNLWKQFESNLGIEIKA-----LDENGH-----DLAVTF	241	
Db	196	---WLSFDVTGVVQWLRSRGEGIEGFLSAHSCDSRDNTLQVDINGFTTGRGDLATI-	251	
QY	242	PGEGEGDLN-PFLEVKVTTPK-----RSRDFGLDCDEHSTESCRCYPLTVDF-BA	292	
Db	252	-----HGMNRPFLMLMATPLERAQHLQSRHRRALDNTNYCFSTKNCVCRQLYIDPRK	306	
QY	293	FGWDWIIAPKRYKANYCSGCEPFVLPQKYPHTH---LVHOANPRGSAGPCCTPTKMSPIN	349	

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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds  
(without alignments)  
2359.729 Million cell updates/sec

Title: US-09-628-112-2

Perfect score: 2018

Sequence: 1 MQKLQICVYILFMLIVAGP.....KEQIYKIPAMVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA\_Main:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap:\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap:\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap:\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	375	3	US-09-454-540-5
2	2018	100.0	375	3	US-09-859-211-14
3	2018	100.0	375	3	US-09-841-730-2
4	2018	100.0	375	3	US-09-872-856-14
5	2018	100.0	375	3	US-09-871-604-5
6	2018	100.0	375	4	US-10-074-152-29
7	2018	100.0	375	4	US-10-278-803-14
8	2018	100.0	375	4	US-10-071-499A-1
9	2018	100.0	375	4	US-10-335-483-14
10	2018	100.0	375	4	US-10-251-115-8
11	2018	100.0	375	4	US-10-253-532-130
12	2018	100.0	375	4	US-10-366-345-51
13	2018	100.0	375	4	US-10-463-973-14
14	2018	100.0	375	4	US-10-456-852-4
15	2018	100.0	375	4	US-10-459-127-5
16	2018	100.0	375	4	US-10-662-438-2
17	2018	100.0	375	5	US-10-689-677C-2
18	2018	100.0	375	5	US-10-665-374-2
19	2018	100.0	375	5	US-10-997-809-14
20	2018	100.0	375	5	US-10-991-343-14
21	2018	100.0	375	6	US-11-019-001-1
22	2018	100.0	376	3	US-09-813-398-38
23	2018	100.0	376	5	US-10-826-324-58
24	2013	99.8	375	3	US-09-859-894A-5
25	2009	99.6	375	4	US-10-278-803-19
26	2008	99.5	375	3	US-09-859-211-19
27	2008	99.5	375	3	US-09-841-730-10

28	2008	99.5	375	3	US-09-872-856-19	Sequence 19, Appl
29	2008	99.5	375	4	US-10-074-152-30	Sequence 30, Appl
30	2008	99.5	375	4	US-10-463-973-19	Sequence 19, Appl
31	2008	99.5	375	4	US-10-456-852-6	Sequence 6, Appl
32	1979	98.1	375	3	US-09-859-211-29	Sequence 29, Appl
33	1979	98.1	375	3	US-09-841-730-14	Sequence 14, Appl
34	1979	98.1	375	3	US-09-872-856-29	Sequence 29, Appl
35	1979	98.1	375	4	US-10-463-973-29	Sequence 29, Appl
36	1976	97.9	375	4	US-10-074-152-32	Sequence 11, Appl
37	1953	96.8	376	3	US-09-859-894A-11	Sequence 12, Appl
38	1953	96.8	376	3	US-09-859-211-12	Sequence 4, Appl
39	1953	96.8	376	3	US-09-841-730-4	Sequence 12, Appl
40	1953	96.8	376	3	US-09-872-856-12	Sequence 12, Appl
41	1953	96.8	376	3	US-09-871-604-10	Sequence 10, Appl
42	1953	96.8	376	4	US-10-074-152-27	Sequence 27, Appl
43	1953	96.8	376	4	US-10-278-803-12	Sequence 12, Appl
44	1953	96.8	376	4	US-10-335-483-12	Sequence 12, Appl
45	1953	96.8	376	4	US-10-251-115-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-09-454-540-5  
; Sequence 5, Application US/09454540  
; Patent No. US20010053358A1  
; GENERAL INFORMATION:  
; APPLICANT: Se-Jin Lee and Alexandra McPherron  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/454,540  
FILING DATE: 06-DEC-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/795,671  
FILING DATE: February 6, 1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: HALL, PH.D., LISA A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/106001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: GDF-8  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..375  
US-09-454-540-5  
Query Match 100.0%; Score 2018; DB 3; Length 375;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds  
(without alignments)  
1694.174 Million cell updates/sec

Title: US-09-628-112-2  
Perfect score: 2018  
Sequence: 1 MQLQLCVIYLFMLIVAGP.....KEQIIYKIPAMVDRGCS 375

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/iaa/6 COMB.pdp:\*  
3: /cgn2\_6/prodata/1/iaa/H\_COMB.pdp:\*  
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6: /cgn2\_6/prodata/1/iaa/backfiles1.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	375	1 US-08-525-596B-14	Sequence 14, Appl
2	2018	100.0	375	1 US-08-765-875-5	Sequence 5, Appl
3	2018	100.0	375	2 US-08-795-671-5	Sequence 5, Appl
4	2018	100.0	375	2 US-09-177-860A-14	Sequence 14, Appl
5	2018	100.0	375	2 US-09-252-149B-29	Sequence 29, Appl
6	2018	100.0	375	2 US-09-378-238-14	Sequence 14, Appl
7	2018	100.0	375	2 US-09-451-501-14	Sequence 14, Appl
8	2018	100.0	375	2 US-09-629-938-14	Sequence 14, Appl
9	2018	100.0	375	2 US-09-454-540-5	Sequence 5, Appl
10	2018	100.0	375	2 US-09-686-344-14	Sequence 2, Appl
11	2018	100.0	375	2 US-09-626-896-2	Sequence 2, Appl
12	2018	100.0	375	2 US-09-485-046-4	Sequence 4, Appl
13	2018	100.0	375	2 US-10-278-803-14	Sequence 14, Appl
14	2018	100.0	375	2 US-09-841-730-2	Sequence 2, Appl
15	2009	99.6	375	2 US-09-451-501-19	Sequence 19, Appl
16	2009	99.6	375	2 US-10-278-803-19	Sequence 19, Appl
17	2008	99.5	375	2 US-09-252-149B-30	Sequence 30, Appl
18	2008	99.5	375	2 US-09-686-344-19	Sequence 19, Appl
19	2008	99.5	375	2 US-09-626-896-10	Sequence 10, Appl
20	2008	99.5	375	2 US-09-485-046-6	Sequence 6, Appl
21	2008	99.5	375	2 US-09-841-730-10	Sequence 10, Appl
22	1979	98.1	375	2 US-09-686-344-29	Sequence 29, Appl
23	1979	98.1	375	2 US-09-626-896-14	Sequence 14, Appl
24	1979	98.1	375	2 US-09-841-730-14	Sequence 14, Appl
25	1976	97.9	375	2 US-09-252-149B-32	Sequence 32, Appl
26	1953	96.8	376	1 US-08-525-596B-12	Sequence 12, Appl
27	1953	96.8	376	2 US-09-177-860A-12	Sequence 12, Appl

28 1953 96.8 376 2 US-08-891-789B-6 Sequence 6, Appl  
29 1953 96.8 376 2 US-09-252-149B-27 Sequence 27, Appl  
30 1953 96.8 376 2 US-09-378-238-12 Sequence 12, Appl  
31 1953 96.8 376 2 US-09-451-501-12 Sequence 12, Appl  
32 1953 96.8 376 2 US-09-629-938-12 Sequence 12, Appl  
33 1953 96.8 376 2 US-09-686-344-12 Sequence 12, Appl  
34 1953 96.8 376 2 US-09-626-896-4 Sequence 4, Appl  
35 1953 96.8 376 2 US-09-485-046-2 Sequence 2, Appl  
36 1953 96.8 376 2 US-10-278-803-12 Sequence 12, Appl  
37 1953 96.8 376 2 US-09-841-730-4 Sequence 4, Appl  
38 1925 95.4 376 2 US-09-252-149B-28 Sequence 28, Appl  
39 1925 95.4 376 2 US-09-451-501-25 Sequence 25, Appl  
40 1925 95.4 376 2 US-09-686-344-25 Sequence 25, Appl  
41 1925 95.4 376 2 US-09-626-896-6 Sequence 6, Appl  
42 1925 95.4 376 2 US-09-485-046-12 Sequence 12, Appl  
43 1925 95.4 376 2 US-10-278-803-25 Sequence 25, Appl  
44 1925 95.4 376 2 US-09-841-730-6 Sequence 6, Appl  
45 1917 95.0 375 2 US-09-686-344-31 Sequence 31, Appl

ALIGNMENTS

RESULT 1  
US-08-525-596B-14  
; Sequence 14, Application US/08525596B  
; Patent No. 5827733  
; GENERAL INFORMATION:  
; APPLICANT: Huynh, Thanh  
; APPLICANT: Lee, Se-Jin  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/525,596B  
; FILING DATE: 19-SEP-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07762  
; FILING DATE: 08-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wetherell, Jr., Ph.D, John R.  
; REGISTRATION NUMBER: 31,678  
; REFERENCE/DOCKET NUMBER: 07265/075001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-678-5070  
; TELEFAX: 619-678-5099  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 375 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-08-525-596B-14

Query Match 100.0%; Score 2018; DB 1; Length 375;  
Best Local Similarity 100.0%; Pred. No. 4.4e-190;  
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQLQLCVIYLFMLIVAGPVDLNENSEQENVEKGLCHACTWRQTKSRIEAIKQI 60  
|||||

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds  
(without alignments)  
1694.174 Million cell updates/sec

Title: US-09-628-112-10

Perfect score: 2016

Sequence: 1 MQKQLCVIYLFMLIVAGP.....KEQIIYKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/1aa/5 COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/H COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/PCTUS COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/RE COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2016	100.0	375	2	US-09-686-344-19
3	2016	100.0	375	2	US-09-626-896-10
4	2016	100.0	375	2	US-09-485-046-6
5	2016	100.0	375	2	US-09-841-730-10
6	2008	99.6	375	1	US-08-525-596B-14
7	2008	99.6	375	1	US-08-765-875-5
8	2008	99.6	375	2	US-08-795-671-5
9	2008	99.6	375	2	US-09-177-860A-14
10	2008	99.6	375	2	US-09-252-149B-29
11	2008	99.6	375	2	US-09-378-238-14
12	2008	99.6	375	2	US-09-451-501-14
13	2008	99.6	375	2	US-09-629-938-14
14	2008	99.6	375	2	US-09-454-540-5
15	2008	99.6	375	2	US-09-686-344-14
16	2008	99.6	375	2	US-09-626-896-2
17	2008	99.6	375	2	US-09-485-046-4
18	2008	99.6	375	2	US-10-278-803-14
19	2008	99.6	375	2	US-09-841-730-2
20	2007	99.6	375	2	US-09-451-501-19
21	2007	99.6	375	2	US-10-278-803-19
22	1977	98.1	375	2	US-09-686-344-29
23	1977	98.1	375	2	US-09-626-896-14
24	1977	98.1	375	2	US-09-841-730-14
25	1974	97.9	375	2	US-09-252-149B-32
26	1951	96.8	376	1	US-08-525-596B-12
27	1951	96.8	376	2	US-09-177-860A-12

28	1951	96.8	376	2	US-08-891-789B-6	Sequence 6, Appli
29	1951	96.8	376	2	US-09-252-149B-27	Sequence 27, Appl
30	1951	96.8	376	2	US-09-378-238-12	Sequence 12, Appl
31	1951	96.8	376	2	US-09-451-501-12	Sequence 12, Appl
32	1951	96.8	376	2	US-09-629-938-12	Sequence 12, Appl
33	1951	96.8	376	2	US-09-686-344-12	Sequence 12, Appl
34	1951	96.8	376	2	US-09-626-896-4	Sequence 4, Appli
35	1951	96.8	376	2	US-09-485-046-2	Sequence 2, Appli
36	1951	96.8	376	2	US-10-278-803-12	Sequence 12, Appl
37	1951	96.8	376	2	US-09-841-730-4	Sequence 4, Appli
38	1923	95.4	376	2	US-09-252-149B-28	Sequence 28, Appl
39	1923	95.4	376	2	US-09-451-501-25	Sequence 25, Appl
40	1923	95.4	376	2	US-09-686-344-25	Sequence 25, Appl
41	1923	95.4	376	2	US-09-626-896-6	Sequence 6, Appli
42	1923	95.4	376	2	US-09-485-046-12	Sequence 12, Appl
43	1923	95.4	376	2	US-10-278-803-25	Sequence 25, Appl
44	1923	95.4	376	2	US-09-841-730-6	Sequence 6, Appli
45	1915	95.0	375	2	US-09-686-344-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1  
US-09-252-149B-30  
; Sequence 30, Application US/09252149B  
; Patent No. 6369201  
; GENERAL INFORMATION:  
; APPLICANT: Barker, Christopher A.  
; APPLICANT: Morsey, Mohamad  
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN  
; FILE OF INVENTION: VERTEBRATE SUBJECTS  
; FILE REFERENCE: 9001-0042  
; CURRENT APPLICATION NUMBER: US/09/252,149B  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: 60/075,213  
; PRIOR FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Papio hamadryas  
US-09-252-149B-30

Query Match Similarity 100.0%; Score 2016; DB 2; Length 375;  
Best Local Similarity 100.0%; Pred. No. 1.4e-195;  
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQKQLCVIYLFMLIVAGPVDLNENSEQENVEKGLCNACTWRONTKSSRIEAIKIQI	60
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Qy	61	LSKRLTAPNISKDAIRQLLPKAPPLRELIQYDVQRDDSDGSLDDDDYHATTETIIT	120
Db	61	LSKRLTAPNISKDAIRQLLPKAPPLRELIQYDVQRDDSDGSLDDDDYHATTETIIT	120
Qy	121	MPTESDFLMQVGGPKCCFFKFSKIQYNKVKAQLMIYLRPVETPTTVFVQILRLIKPM	180
Db	121	MPTESDFLMQVGGPKCCFFKFSKIQYNKVKAQLMIYLRPVETPTTVFVQILRLIKPM	180
Qy	181	KDGRYTGIRSLKLDMPGPGIWSIDVKTVLQNLKOPESNLGIEIKALDENGHLAVT	240
Db	181	KDGRYTGIRSLKLDMPGPGIWSIDVKTVLQNLKOPESNLGIEIKALDENGHLAVT	240
Qy	241	FPGEGDGLNPFLEVKVYTDTPKSRDRFGLDCDSEHSTESRCRYPYLVDFEALGWDWIIA	300
Db	241	FPGEGDGLNPFLEVKVYTDTPKSRDRFGLDCDSEHSTESRCRYPYLVDFEALGWDWIIA	300
Qy	301	PKRYKANCSECEBFVFLQKYPHTLHVQANPRGSAGCCTPTTKXSPINMLYFNGKEQII	360
Db	301	PKRYKANCSECEBFVFLQKYPHTLHVQANPRGSAGCCTPTTKXSPINMLYFNGKEQII	360

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3488 Seconds  
(without alignments)  
1694.174 Million cell updates/sec

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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues  
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/1/aaa/6 COMB.pdp.\*  
3: /cgn2\_6/ptodata/1/aaa/H COMB.pdp.\*  
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5: /cgn2\_6/ptodata/1/aaa/RB COMB.pdp.\*  
6: /cgn2\_6/ptodata/1/aaa/backfiles1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2019	100.0	376	2	US-09-252-149B-28
2	2019	100.0	376	2	US-09-451-501-25
3	2019	100.0	376	2	US-09-626-896-6
4	2019	100.0	376	2	US-09-485-046-12
5	2019	100.0	376	2	US-10-278-803-25
6	2019	100.0	376	2	US-09-841-730-6
7	1986	98.4	376	1	US-08-525-596B-12
8	1986	98.4	376	2	US-09-177-860A-12
9	1986	98.4	376	2	US-08-891-789B-6
10	1986	98.4	376	2	US-09-252-149B-27
11	1986	98.4	376	2	US-09-378-238-12
12	1986	98.4	376	2	US-09-451-501-12
13	1986	98.4	376	2	US-09-629-938-12
14	1986	98.4	376	2	US-09-626-896-4
15	1986	98.4	376	2	US-09-625-896-4
16	1986	98.4	376	2	US-09-485-046-2
17	1986	98.4	376	2	US-10-278-803-12
18	1986	98.4	376	2	US-09-841-730-4
19	1986	98.4	376	2	US-09-451-501-19
20	1932	95.7	375	2	US-10-278-803-19
21	1932	95.7	375	2	US-09-252-149B-32
22	1931	95.6	375	2	US-09-626-896-14
23	1928	95.5	375	2	US-09-626-896-14
24	1928	95.5	375	2	US-09-841-730-14
25	1928	95.5	375	1	US-08-525-596B-14
26	1925	95.3	375	1	US-08-765-875-5
27	1925	95.3	375	1	US-08-765-875-5

28	1925	95.3	375	2	US-08-795-671-5	Sequence 5, Appl
29	1925	95.3	375	2	US-09-177-860A-14	Sequence 14, Appl
30	1925	95.3	375	2	US-09-252-149B-29	Sequence 29, Appl
31	1925	95.3	375	2	US-09-378-238-14	Sequence 14, Appl
32	1925	95.3	375	2	US-09-451-501-14	Sequence 14, Appl
33	1925	95.3	375	2	US-09-629-938-14	Sequence 14, Appl
34	1925	95.3	375	2	US-09-454-540-5	Sequence 5, Appl
35	1925	95.3	375	2	US-09-686-344-14	Sequence 14, Appl
36	1925	95.3	375	2	US-09-626-896-2	Sequence 2, Appl
37	1925	95.3	375	2	US-09-485-046-4	Sequence 4, Appl
38	1925	95.3	375	2	US-10-278-803-14	Sequence 14, Appl
39	1925	95.3	375	2	US-09-841-730-2	Sequence 2, Appl
40	1923	95.2	375	2	US-09-252-149B-30	Sequence 30, Appl
41	1923	95.2	375	2	US-09-686-344-19	Sequence 19, Appl
42	1923	95.2	375	2	US-09-626-896-10	Sequence 10, Appl
43	1923	95.2	375	2	US-09-485-046-6	Sequence 6, Appl
44	1923	95.2	375	2	US-09-841-730-10	Sequence 10, Appl
45	1865	92.4	375	2	US-09-252-149B-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1  
US-09-252-149B-28  
; Sequence 28, Application US/09252149B  
; Patent No. 6369201  
; GENERAL INFORMATION:  
; APPLICANT: Barker, Christopher A.  
; APPLICANT: Morsey, Mohamed  
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN  
; FILE REFERENCE: 9001-0042  
; CURRENT APPLICATION NUMBER: US/09/252.149B  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: 60/075.213  
; PRIOR FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; US-09-252-149B-28

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Matches	376;	Conservative	0;	Mismatches	0;	Gaps	0;
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Db	1	MIQKPMQVYIYLFVLIAGPVDL	NEDSREANVEKEGLCNACAWQNT	RYSR	IAIKIQ	60	
QY	61	ILSKRLTETAPNISKDAIRQLPRAP	PLRELIDQYVQRDDSDGSL	EDDYHATTETII	120		
Db	61	ILSKRLTETAPNISKDAIRQLPRAP	PLRELIDQYVQRDDSDGSL	EDDYHATTETII	120		
QY	121	TMPTESDPLMQADGPKCCFPKFSKIQYNKVKQAQWL	YLVRAVKTPTTFVQILRLKP	180			
Db	121	TMPTESDPLMQADGPKCCFPKFSKIQYNKVKQAQWL	YLVRAVKTPTTFVQILRLKP	180			
QY	181	MDGTRTYGIRSLKLDMSPGTGIWQSDVKTVLQWL	KQPSNLGIEIKALDENGHD	240			
Db	181	MDGTRTYGIRSLKLDMSPGTGIWQSDVKTVLQWL	KQPSNLGIEIKALDENGHD	240			
QY	241	TFPGFGEDGLNPFLEVKVTDTPKSRDRFGDCCD	DEHSTESCRCRYPL	VDFFAFCWDMII	300		
Db	241	TFPGFGEDGLNPFLEVKVTDTPKSRDRFGDCCD	DEHSTESCRCRYPL	VDFFAFCWDMII	300		
QY	301	APKRYKANYCSGECEFFVLOKYPHTLVHQA	NPRGSAGPCCTPTKMS	PINMLYFNKGKQI	360		
Db	301	APKRYKANYCSGECEFFVLOKYPHTLVHQA	NPRGSAGPCCTPTKMS	PINMLYFNKGKQI	360		